PCT WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 6 : C07H 21/00, 21/02, 21/04, C12N 15/09, C12Q 1/68 — A1

(11) International Publication Number: **WO 98/24796**

(43) International Publication Date: 11 June 1998 (11.06.98)

(21) International Application Number: PCT/US97/21782

(22) International Filing Date: 1 December 1997 (01.12.97)

(30) Priority Data:

60/032,069	2 December 1996 (02.12.96)	US
08/813,507	7 March 1997 (07.03.97)	US

(71) Applicant *(for all designated States except US)*: AFFYMETRIX INCORPORATED [US/US]; 3380 Central Expressway, Santa Clara, CA 95051 (US).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: LEMIEUX, Bertrand [CA/CA]; 2164 Dickson Street, Sillery, Quebec G1T 1C9 (CA). LANDRY, Benoit, S. [CA/CA]; 134 Allée des Cigales, Lacadie, Quebec J2Y 1B3 (CA). SAPOLSKY, Ronald, J. [US/US]; 1945 Latham Street #3, Mountain View, CA 94040 (US). MURIGNEUX, Alain [FR/FR]; 24, avenue des Landais, F–63170 Aubière (FR).

(74) Agents: LIEBESCHUETZ, Joe et al.; Townsend and Townsend and Crew LLP, 8th floor, Two Embarcadero Center, San Francisco, CA 94111–3834 (US).

(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).

Published

With international search report.

Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.

(54) Title: BRASSICA POLYMORPHISMS

(57) Abstract

The invention provides oligonucleotides and their complements that can be used as allele–specific probes or primers for sequencing, oligonucleotide probe hybridization, and allele–specific amplification. Such oligonucleotides can be used, for example, to facilitate genetic distinction between individual plants in plant populations.

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	**ES**	Spain	**LS**	Lesotho	**SI**	Slovenia
AM	Armenia	**FI**	Finland	**LT**	Lithuania	**SK**	Slovakia
AT	Austria	**FR**	France	**LU**	Luxembourg	**SN**	Senegal
AU	Australia	**GA**	Gabon	**LV**	Latvia	**SZ**	Swaziland
AZ	Azerbaijan	**GB**	United Kingdom	**MC**	Monaco	**TD**	Chad
BA	Bosnia and Herzegovina	**GE**	Georgia	**MD**	Republic of Moldova	**TG**	Togo
BB	Barbados	**GH**	Ghana	**MG**	Madagascar	**TJ**	Tajikistan
BE	Belgium	**GN**	Guinea	**MK**	The former Yugoslav Republic of Macedonia	**TM**	Turkmenistan
BF	Burkina Faso	**GR**	Greece			**TR**	Turkey
BG	Bulgaria	**HU**	Hungary	**ML**	Mali	**TT**	Trinidad and Tobago
BJ	Benin	**IE**	Ireland	**MN**	Mongolia	**UA**	Ukraine
BR	Brazil	**IL**	Israel	**MR**	Mauritania	**UG**	Uganda
BY	Belarus	**IS**	Iceland	**MW**	Malawi	**US**	United States of America
CA	Canada	**IT**	Italy	**MX**	Mexico	**UZ**	Uzbekistan
CF	Central African Republic	**JP**	Japan	**NE**	Niger	**VN**	Viet Nam
CG	Congo	**KE**	Kenya	**NL**	Netherlands	**YU**	Yugoslavia
CH	Switzerland	**KG**	Kyrgyzstan	**NO**	Norway	**ZW**	Zimbabwe
CI	Côte d'Ivoire	**KP**	Democratic People's Republic of Korea	**NZ**	New Zealand		
CM	Cameroon			**PL**	Poland		
CN	China	**KR**	Republic of Korea	**PT**	Portugal		
CU	Cuba	**KZ**	Kazakstan	**RO**	Romania		
CZ	Czech Republic	**LC**	Saint Lucia	**RU**	Russian Federation		
DE	Germany	**LI**	Liechtenstein	**SD**	Sudan		
DK	Denmark	**LK**	Sri Lanka	**SE**	Sweden		
EE	Estonia	**LR**	Liberia	**SG**	Singapore		

BRASSICA POLYMORPHISMS

COPYRIGHT NOTICE

CROSS-REFERENCE TO RELATED APPLICATION

The present application is a continuation in part of USSN 08/813,507, filed March 7, 1997, which derives priority from provisional application 60/032,069, filed December 2, 1996, both of which are incorporated by reference in its entirety for all purposes.

BACKGROUND OF THE INVENTION

The genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution generating variant forms of progenitor sequences (Gusella, *Ann. Rev. Biochem.* 55, 831-854 (1986)). The variant form may confer an evolutionary advantage or disadvantage relative to a progenitor form or may be neutral. In some instances, a variant form confers a lethal disadvantage and is not transmitted to subsequent generations of the organism. In other instances, a variant form confers an evolutionary advantage to the species and is eventually incorporated into the DNA of many or most members of the species and effectively becomes the progenitor form. In many instances, both progenitor and variant form(s) survive and co-exist in a species population. The coexistence of multiple forms of a sequence gives rise to polymorphisms.

Several different types of polymorphism have been reported. A restriction fragment length polymorphism (RFLP) means a variation in DNA sequence that alters the length of a restriction fragment as described in Botstein et al., *Am. J. Hum. Genet.* 32, 314-331 (1980). The restriction fragment length polymorphism may create or delete a restriction site, thus changing the length of the restriction fragment. RFLPs have been widely used in human and animal genetic analyses (see WO 90/13668; W090/11369; Donis-Keller, *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 85-99 (1989)). When a heritable trait can be linked to a particular RFLP, the presence of the RFLP in an individual can be used to predict the likelihood that the animal will also exhibit the trait.

Other polymorphisms take the form of short tandem repeats (STRs) that include tandem di-, tri- and tetra-nucleotide repeated motifs. These tandem repeats are also referred to as variable number tandem repeat (VNTR) polymorphisms. VNTRs have been used in identity and paternity analysis (US 5,075,217; Armour et al., *FEBS Lett.* 307, 113-115 (1992); Horn et al., W0 91/14003; Jeffreys, EP 370,719), and in a large number of genetic mapping studies.

Other polymorphisms take the form of single nucleotide variations between individuals of the same species. Such polymorphisms are far more frequent than RFLPs, STRs and VNTRs. Some single nucleotide polymorphisms occur in protein-coding sequences, in which case, one of the polymorphic forms may give rise to the expression of a defective or other variant protein. Other single nucleotide polymorphisms occur in noncoding regions. Some of these polymorphisms may also result in defective or variant protein expression (e.g., as a result of defective splicing). Other single nucleotide polymorphisms have no phenotypic effects. Single nucleotide polymorphisms can be used in the same manner as RFLPs, and VNTRs but offer several advantages. Single nucleotide polymorphisms occur with greater frequency and are spaced more uniformly throughout the genome than other forms of polymorphism. The greater frequency and uniformity of single nucleotide polymorphisms means that there is a greater

probability that such a polymorphism will be found in close proximity to a genetic locus of interest than would be the case for other polymorphisms. Also, the different forms of characterized single nucleotide polymorphisms are often easier to distinguish that other types of polymorphism (e.g., by use of assays employing allele-specific hybridization probes or primers).

Despite the increased amount of nucleotide sequence data being generated in recent years, only a minute proportion of the total repository of polymorphisms has so far been identified. The paucity of polymorphisms hitherto identified is due to the large amount of work required for their detection by conventional methods. For example, a conventional approach to identifying polymorphisms might be to sequence the same stretch of oligonucleotides in a population of individuals by didoxy sequencing. In this type of approach, the amount of work increases in proportion to both the length of sequence and the number of individuals in a population and becomes impractical for large stretches of DNA or large numbers of subjects.

SUMMARY OF THE INVENTION

The invention provides nucleic acid segments containing at least 10, 15 or 20 contiguous bases from a fragment shown in Table 1 or 2, the complement thereof, or a plant cognate variant of the fragment. The segments include a polymorphic site shown in Table 1 or 2. The segments can be DNA or RNA, and can be double- or single-stranded. Some segments are 10-20 or 10-50 bases long. Preferred segments include a diallelic polymorphic site.

The invention further provides allele-specific oligonucleotides that hybridizes to a segment of a fragment shown in Table 1 or 2 or its complement. These oligonucleotides can be probes or primers. Also provided are isolated nucleic acids comprising a sequence of Table 1 or 2 or the complement thereto, in which the polymorphic site within the sequence is occupied by a base other than the reference base shown in Table 1 or 2.

The invention further provides a method of analyzing a nucleic acid from a subject. The method determines which base or bases is/are present at any one of the polymorphic sites shown in Table 1 or 2. Optionally, a set of bases occupying a set of the polymorphic sites shown in Table 1 or 2 is determined. This type of analysis can be performed on a plurality of subjects who are tested for the presence of a phenotype. The presence or absence of phenotype can then be correlated with a base or set of bases present at the polymorphic sites in the subjects tested.

BRIEF DESCRIPTION OF THE FIGURE

Fig. 1 shows probe arrays tiles for two allelic forms of the Brassica 18A2 polymorphism.

DEFINITIONS

A nucleic acid, such an oligonucleotide, oligonucleotide can be DNA or RNA, and single- or double-stranded. Oligonucleotides can be naturally occurring or synthetic, but are typically prepared by synthetic means. Preferred nucleic acids of the invention include segments of DNA, or their complements including any one of the polymorphic sites shown in Table 1 or 2. The segments are usually between 5 and 100 bases, and often between 5-10, 5-20, 10-20, 10-50, 20-50 or 20-100 bases. The polymorphic site can occur within any position of the segment. The segments can be from any of the allelic forms of DNA shown in Table 1 or 2. Methods of synthesizing oligonucleotides are found in, for example, *Oligonucleotide Synthesis: A Practical Approach* (Gait, ed., IRL Press, Oxford, 1984).

Hybridization probes are oligonucleotides capable of binding in a base-specific manner to a complementary strand of nucleic acid. Such probes include peptide nucleic acids, as described in Nielsen et al., *Science* 254, 1497-1500 (1991).

The term primer refers to a single-stranded oligonucleotide capable of acting as a point of initiation of template-directed DNA synthesis under appropriate conditions (*i.e.*, in the presence of four different nucleoside

triphosphates and an agent for polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer but typically ranges from 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template but must be sufficiently complementary to hybridize with a template. The term primer site refers to the area of the target DNA to which a primer hybridizes. The term primer pair means a set of primers including a 5' upstream primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3', downstream primer that hybridizes with the complement of the 3' end of the sequence to be amplified.

Linkage describes the tendency of genes, alleles, loci or genetic markers to be inherited together as a result of their location on the same chromosome, and can be measured by percent recombination between the two genes, alleles, loci or genetic markers.

Polymorphism refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. A polymorphic marker or site is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats, and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as a the reference form and other allelic forms are designated as alternative or variant alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the wildtype form. Diploid organisms may be homozygous

or heterozygous for allelic forms. A diallelic polymorphism has two forms. A triallelic polymorphism has three forms.

A single nucleotide polymorphism occurs at a polymorphic site occupied by a single nucleotide, which is the site of variation between allelic sequences. The site is usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations).

A single nucleotide polymorphism usually arises due to substitution of one nucleotide for another at the polymorphic site. A transition is the replacement of one purine by another purine or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine or vice versa. Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele.

Hybridizations are usually performed under stringent conditions, for example, at a salt concentration of no more than 1 M and a temperature of at least 25°C. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C are suitable for allele-specific probe hybridizations.

The invention provides DNA sequences from Brassica and corn and cognate sequences from other plants. The term cognate refers to a gene sequence that is evolutionarily and functionally related between species. Cognate genes typically exhibit a high degree of sequence identity, (e.g., at least 80, 90, 95 or 99%) and hybridize to each other under stringent conditions. A polymorphic site in cognate sequences occur in corresponding positions when the sequences are maximally aligned according to the criteria of any one of the following references: Smith & Waterman (1981), *Adv. Appl. Math.* 2, 482; Needleman & Wunsch (1970), *J. Mol. Biol.* 48: 443; Pearson & Lipman (1988), *Proc. Natl. Acad. Sci. (U.S.A.)* 85: GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI (each of which is incorporated by reference in its entirety for all purposes).

Nucleic acids of the invention are often in isolated form. An isolated nucleic acid means an object species that is the predominant species present (*i.e.*, on a molar basis it is more abundant than any other individual species in the composition). Preferably, an isolated nucleic acid comprises at least about 50, 80 or 90 percent (on a molar basis) of all macromolecular species present. Most preferably, the object species is purified to essential homogeneity (contaminant species cannot be detected in the composition by conventional detection methods).

DESCRIPTION OF THE PRESENT INVENTION

I. Novel Polymorphisms of the Invention

The present application provides oligonucleotides containing polymorphic sites isolated from two *Brassica* species, *B. napus* and *B. oleracea*, or corn, or cognate sequences from other plants. The invention also includes various methods for using those novel oligonucleotides to identify, distinguish, and determine the relatedness of individual strains or pools of nucleic acids from plants, particularly vegetal plants, and especially plants, within the family *Cruciferae* or *Teosinte*.

The genus *Brassica* is part of the family *Cruciferae*. Members of the *Brassica* genus have been described as Old World Temperate Zone herbs of the mustard family with beaked cylindrical pods. *Merriam-Webster's Collegiate Dictionary*, (10th ed., 1993), p.139. Many cruciferous plants are important agricultural items and include many foodstuffs (condiments, oilseeds, and vegetables). For example, canola (a type of *Brassica napus*) is one of the largest crops in Canada.

Sequences 1-149 in Table 1 and sequences from 86-5B5-N3 to 2B7/2F7-2A in Table 2 were isolated from *B. napus* and *B. oleracea* using oligonucleotide primers designed from expressed DNA sequences from *Arabidopsis thaliana*, a relative of *Brassica napus* and member of the *Cruciferae* family. See Hofte et al., An inventory of expressed sequence tags obtained by partial sequencing of cDNAs from *Arabidopsis thaliana, Plant*

J., Vol.4, pp. 1051-1061 (1993) and Newman et al., Genes Galore: A Summary of Methods for Accessing Results from Large-Scale Partial Sequencing of Anonymous *Arabidopsis* cDNA Clones, *Plant Physiol.*, Vol. 106, pp. 1241-1255 (1994). There is a high degree of homology between the coding sequences of *Arabidopsis, Brassica,* and other members of the *Cruciferae* family.

The designations in Table 1 are as follows. The first column is an arbitrarily assigned identification number for a polymorphism. The second and third columns, xmin and ymin, are the co-ordinates of probes for analyzing the polymorphism on a DNA chip (to be described below). The first number in the marker name is the *Brassica* strain name corresponding to the upper allele sequence. The next number designates the primer pair used for the PCR amplification. The sequences of some primers are described at the web site (*http://www.yorku.ca/ftp/york_other/cgat/*) (incorporated by reference in its entirety for all purposes). The last number is the name of the strain for the lower allele sequence. For example 85/5B5/86-1 means that the polymorphic site was identified by comparing strains 85 and 86-1 at a segment amplified by primers 5B5. Each sequence in the table includes a polymorphic site shown in square brackets [] and flanking bases common to both strains being compared. The upper and lower sequences in the square brackets are from the two strains being compared (upper strand corresponding to the first designated strain). A "/" within square brackets followed or preceded by a blank space represents an addition/deletion polymorphism. An asterisk indicates triallelic markers. The designation N indicates a base whose identity was not determined. The nomenclature for Table 2 is similar except that only fragment names and sequences flanking and including polymorphic sites are shown. In both Tables 1 and 2, the symbol "T" should be read as a "U" in RNA forms of the nucleic acids provided by the invention.

The invention further provides oligonucleotides from corn (zea maize), and cognate sequences from other plants especially those from the *Teosinte* family in which corn falls.

DNA was extracted from maize lines as described in Rogers and Bendich, *Plant Biol. Manual* A6, 1-10 (1988) with modification described in Murigneux et al., *Theo. Appl. Genet.* 86, 837-842 1993). PCR amplification was done on six maize lines representing a wide range of genetic variability and including both European flint material and US dent germplasm. These six maize lines were chosen to maximize genetic variability and thereby improve the probability of finding polymorphisms in the allelic sequences. Preferred primers for amplification of some DNA segments including polymorphic sites are shown in Table 3. Other primers can be designed to incorporate sequences flanking the nucleic acid segments listed in Tables 1 and 2. Flanking sequences can be obtained from GenBank, or Bae et al., *Maydica* 35, 317-322 (1990), or PCR-based gene walking. *See* Parker et al., *Nucl. Acids Res.* 19, 3055-3060. A specific primer for the sequenced region is primed with a general primer that hybridizes to the flanking region.

Nucleic acid segments flanking polymorphic sites in Zea Maize are shown as sequences 150-264 of Table 1, and sequences from S71G2/G6-1 to S01G3/G7-2 in Table 2. The nomenclature is the same as that described earlier for *Brassica sequences*.

II. Analysis of Polymorphisms

A. Preparation of Samples

Polymorphisms are detected in a target nucleic acid from a plant being analyzed. Target nucleic acids can be genomic or cDNA. Many of the methods described below require amplification of DNA from target samples. This can be accomplished by e.g., PCR. *See generally PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., *Nucleic Acids Res.* 19, 4967 (1991); Eckert et al., *PCR Methods and Applications* 1, 17 (1991); *PCR* (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202 (each of which is incorporated by reference for all purposes).

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4, 560 (1989), Landegren et al., *Science* 241, 1077 (1988), transcription amplification (Kwoh et al., *Proc. Natl. Acad. Sci. USA* 86, 1173 (1989)), and self-sustained sequence replication (Guatelli et al., *Proc. Nat. Acad. Sci. USA*, 87, 1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

B. Detection of Polymorphisms in Target DNA

There are two distinct types of analysis depending whether a polymorphism in question has already been characterized. The first type of analysis is sometimes referred to as de novo characterization. This analysis compares target sequences in different individual plants to identify points of variation, i.e., polymorphic sites. The de novo identification of the polymorphisms of the invention is described in the Examples section. The second type of analysis is determining which form(s) of a characterized polymorphism are present in plants under test. There are a variety of suitable procedures, which are discussed in turn.

1. Allele-Specific Probes

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., *Nature* 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one member of a species but do not hybridize to the corresponding segment from another member due to the presence of different polymorphic forms in the respective segments from the two members. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary

response, whereby a probe hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15 mer at the 7 position; in a 16 mer, at either the 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

2. Tiling Arrays

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some example of which are described by WO 95/11995 (incorporated by reference in its entirety for all purposes). One form of such arrays is described in the Examples section in connection with de novo identification of polymorphisms. The same array or a different array can be used for analysis of characterized polymorphisms. WO 95/11995 also describes subarrays that are optimized for detection of a variant forms of a precharacterized polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles as described in the Examples except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particular useful for analyzing short subsequences of the primary reference sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (*i.e.*, two or more mutations within 9 to 21 bases).

A DNA chip has been designed containing subarrays of probes for analyzing each of the 264 polymorphic sites shown

in Table 1. Preferred polymorphic sites for inclusion on such a chip are selected by a number of criteria. Some polymorphic sites are selected because they are evenly distributed throughout the genome of a plant. For example, one or more polymorphisms is present on each chromosome. Preferably, the polymorphisms are no more than 20 cM apart. Other polymorphisms are selected because they occur within a segment that can be made to give a single band on Southern analysis. Other polymorphisms may be selected because they occur in genes encoding enzymes that function in the same pathway.

Preferred primer pairs for amplification of nucleic acid segments flanking most of these polymorphic sites of Table 1 are shown in Table 3. This chip is used to determine a polymorphic profile of a plant under test at some or all of the polymorphic sites on the chip. Thus, one can determine which allelic form is present in a plant at up to 264 sites. Such a profile is useful in some of the applications described below.

DNA segments are preferably amplified in a multiplex fashion. For example, polymorphic sites 5, 8, 64, 108, 36, 38, and 136 (Table 1) can be amplified from the primers shown in Table 3 in one group. Polymorphic sites 11, 12, 15, 29, 130, 139, 140, 40, 49, 63, 72, 81, 86, 92, 93, 102, 142, 146, 149, 16, 138 can be amplified in another group. Polymorphic sites 1, 7, 17, 25, 26, 42, 60, 67, 73, 75, 106, 107, 111, 123, 133, 43, 51, 82, 95, and 101 can be amplified in another group. Polymorphic sites 2, 9, 20, 34, 41, 45, 61, 62, 65, 74, 75, 80, 91, 100, 105, 110, 123, and 14 can be amplified in another group. Polymorphic sites 4, 41, 61, 62, 65, 66, 76, 80, 91, 94, 111, 114, 121, 132, 22, 32, 33, 44, 53, 97 and 145 can be amplified in another group. Polymorphic sites 6, 21, 27, 46, 66, 68, 71, 77, 89, 89, 98, 103, 105, 31, 35, 54, 59, 84, 85, 96, 116, 137, 141, and 148 can be amplified in another group. Polymorphic sites 48, 70, 78, 87, 88, 90, 99, 103, 104, 112, 117, 118, 119, 122, 124, 13, 18, 30, 37, 69, 94, 135, and 147 can be amplified in another group. Polymorphic sites 247, 207, 203, and 173 can be amplified in another group. Polymorphic sites 229, 217, 212, 204, 195, 171, 175,

236, 174, and 193 can be amplified in another group. Polymorphic sites 232, 243, 157, 162, 169, 177, 179, 234, 241, 255, 152, 160, 184, 188, 192, 199, 201, 205, 210, 220, 223, 226, 245, 249, and 252 can be amplified in another group. Polymorphic sites 233, 244, 246, 248, 227, 211, 214, 200, 150, 158, 170, 178, 181, 238, 254, 161, 165, 180, 187, 222, and 231 can be amplified from another group. Polymorphic sites 228, 235, 215, 218, 221, 225, 198, 155, 163, 166, 167, 172, 216, 242, 159, 182, 186, 191, 202, 208, 230, 237, and 253 can be amplified in another group. Polymorphic sites 219, 224, 206, 209, 213, 194, 196, 197, 151, 153, 156, 164, 185, 250, 154, 168, 176, 183, 190, 239, 251, and 256 can be amplified in another group.

3. Allele-Specific Primers

An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two primers leading to a detectable product signifying the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer. *See, e.g.*, WO 93/22456.

4. Direct-Sequencing

The direct analysis of the sequence of polymorphisms of the present invention can be accomplished using either the dideoxy chain termination method or the Maxam Gilbert method (see Sambrook et al., *Molecular Cloning, A*

Laboratory Manual (2nd Ed., CSHP, New York 1989); Zyskind et al., *Recombinant DNA Laboratory Manual*, (Acad. Press, 1988)).

5. Denaturing Gradient Gel Electrophoresis

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., *PCR Technology, Principles and Applications for DNA Amplification*, (W.H. Freeman and Co, New York, 1992), Chapter 7.

6. Single-Strand Conformation Polymorphism Analysis

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., *Proc. Nat. Acad. Sci.* 86, 2766-2770 (1989). Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence difference between alleles of target sequences.

III. Methods of Use

After determining polymorphic form(s) present in a subject plant at one or more polymorphic sites, this information can be used in a number of methods.

A. Fingerprint Analysis

Analysis of which polymorphisms are present in a plant is useful in determining of which strain the plant is a member an in distinguishing one strain from another. A genetic fingerprint for an individual strain can be made by determining the nucleic acid sequence possessed by that

individual strain that corresponds to a region of the genome known to contain polymorphisms. For a discussion of genetic fingerprinting in the animal kingdom, see, for example, Stokening et.al., *Am. J. Hum. Genet.* 48:370-382 (1991). The probability that one or more polymorphisms in an individual strain is the same as that in any other individual strain decreases as the number of polymorphic sites is increased.

The comparison of the nucleic acid sequences from two strains at one or multiple polymorphic sites can also demonstrate common or disparate ancestry. Since the polymorphic sites are within a large region in the genome, the probability of recombination between these polymorphic sites is low. That low probability means the haplotype (the set of all the disclosed polymorphic sites) set forth in this application should be inherited without change for at least several generations. Knowledge of plant strain or ancestry is useful, for example, in a plant breeding program or in tracing progeny of a proprietary plant. Fingerprints are also used to identify an individual strain and to distinguish or determine the relatedness of one individual strain to another. Genetic fingerprinting can also be useful in hybrid certification, the certification of seed lots, and the assertion of plant breeders rights under the laws of various countries.

Genetic fingerprinting is also useful in screening progeny of a backcross for a high contribution of a parent strain (see Hospital et al., *Genetics* 44, 843-874 (1992)). In a backcross, a progeny that has been bred to have a desired phenotype is crossed with a parental strain to remove genetic variations that do not contribute to the desired phenotype but which may have latent undesirable effects. After crossing, offspring retaining the desired phenotype are identified, and their polymorphic profile is determined. The offspring retaining the desired phenotype and having the greatest similarity in polymorphic profile to a parent strain can then used as a production model.

B. Correlation of Polymorphisms with Phenotypic Traits

The polymorphisms of the invention may contribute to the phenotype of a plant in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the circumstances. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose a plant to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include characteristics such as growth rate, crop yield, crop quality, resistance to pathogens, herbicides, and other toxins, nutrient requirements, resistance to high temperature, freezing, drought, requirements for light and soil type, aesthetics, and height. Other phenotypic traits include susceptibility or resistance to diseases, such as plant cancers. Often polymorphisms occurring within the same gene correlate with the same phenotype.

Correlation is performed for a population of plants, which have been tested for the presence or absence of a phenotypic trait of interest and for polymorphic markers sets. To perform such analysis, the presence or absence of a set of polymorphisms (i.e. a polymorphic set) is determined for a set of the plants, some of whom exhibit a particular trait, and some of which exhibit lack of the trait. The alleles of each polymorphism of the set are then reviewed to determine whether the presence or absence of a particular allele is associated with the trait of interest. Correlation can be performed by standard statistical methods such as a κ-squared test and statistically significant correlations between polymorphic form(s) and phenotypic characteristics are noted.

Correlations between characteristics and phenotype are useful for breeding for desired characteristics. By analogy, Beitz et al., US 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wildtype with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered. Each production trait was analyzed individually with the following animal model:

$$Y_{ijkpn} = \mu + YS_i + P_j + X_k + \beta_1 + \ldots \beta_{17} + PE_n + a_n + e_p$$

where Y_{ijknp} is the milk, fat, fat percentage, SNF, SNF percentage, energy concentration, or lactation energy record; μ is an overall mean; YS_i is the effect common to all cows calving in year-season; X_k is the effect common to cows in either the high or average selection line; β_1 to β_{17} are the binomial regressions of production record on mtDNA D-loop sequence polymorphisms; PE_n is permanent environmental effect common to all records of cow n; a_n is effect of animal n and is composed of the additive genetic contribution of sire and dam breeding values and a Mendelian sampling effect; and e_p is a random residual. It was found that eleven of seventeen polymorphisms tested influenced at least one production trait. Bovines having the best polymorphic forms for milk production at these eleven loci are used as parents for breeding the next generation of the herd.

One can test at least several hundreds of markers simultaneously in order to identify those linked to a gene or chromosomal region. For example, to identify markers linked to a gene conferring disease resistance, a DNA pool is constructed from plants of a segregating population that are resistant and another pool is constructed from plants that are sensitive to the disease. Those two DNA pools are identical except for the DNA sequences at the resistance gene locus and in the surrounding genomic area. Hybridization of such DNA pools to the DNA sequences listed in Table 1 allows the simultaneous testing of several hundreds of loci for polymorphisms. Allelic polymorphism-detecting sequences that

show differences in hybridization patterns between such DNA pools represent loci linked to the disease resistance gene.

The method just described can also be applied to rapidly identify rare alleles in large populations of plants. For example, nucleic acid pools are constructed from several individuals of a large population. The nucleic acid pools are hybridized to nucleic acids having the polymorphism-detecting sequences listed in Table 1 or 2. The detection of a rare hybridization profile will indicate the presence of a rare allele in a specific nucleic acid pool. RNA pools are particularly suited to identify differences in gene expression.

IV. Modified Polypeptides and Gene Sequences

The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise at least 10 contiguous bases of one of the sequences described in Table 1 or 2, in any of the allelic forms shown. Some nucleic acid encode full-length proteins.

Genes can be expressed in an expression vector in which a gene is operably linked to a native or other promoter. Usually, the promoter is a eukaryotic promoter for expression in a eukaryotic cell. The transcription regulation sequences typically include a heterologous promoter and optionally an enhancer which is recognized by the host. The selection of an appropriate promoter, for example trp, lac, phage promoters, glycolytic enzyme promoters and tRNA promoters, depends on the host selected. Commercially available expression vectors can be used. Vectors can include host-recognized replication systems, amplifiable genes, selectable markers, host sequences useful for insertion into the host genome, and the like.

The means of introducing the expression construct into a host cell varies depending upon the particular construction and the target host. Suitable means include fusion, conjugation, transfection, transduction, electroporation or injection, as described in Sambrook, *supra*. A wide variety of host cells can be employed for expression of the variant gene, both prokaryotic and eukaryotic. Suitable host cells include

bacteria such as *E. coli*, yeast, filamentous fungi, insect cells, mammalian cells, typically immortalized, *e.g.*, mouse, CHO, human and monkey cell lines and derivatives thereof, and plant cells. Preferred host cells are able to process the variant gene product to produce an appropriate mature polypeptide. Processing includes glycosylation, ubiquitination, disulfide bond formation, general post-translational modification, and the like.

The DNA fragments are introduced into cultured plant cells by standard methods including electroporation (From et al., *Proc. Natl Acad. Sci. USA* 82, 5824 (1985), infection by viral vectors such as cauliflower mosaic virus (CaMV) (Hohn et al., *Molecular Biology of Plant Tumors*, (Academic Press, New York, 1982) pp. 549-560; Howell, US 4,407,956), high velocity ballistic penetration by small particles with the nucleic acid either within the matrix of small beads or particles, or on the surface (Klein et al., *Nature* 327, 70-73 (1987)), use of pollen as vector (WO 85/01856), or use of *Agrobacterium tumefaciens* transformed with a Ti plasmid in which DNA fragments are cloned. The Ti plasmid is transmitted to plant cells upon infection by *Agrobacterium tumefaciens*, and is stably integrated into the plant genome (Horsch et al., *Science*, 233, 496-498 (1984); Fraley et al., *Proc. Natl. Acad. Sci. USA* 80, 4803 (1983)).

The protein may be isolated by conventional means of protein biochemistry and purification to obtain a substantially pure product, *i.e.*, 80, 95 or 99% free of cell component contaminants, as described in Jacoby, *Methods in Enzymology* Volume 104, Academic Press, New York (1984); Scopes, *Protein Purification, Principles and Practice*, 2nd Edition, Springer-Verlag, New York (1987); and Deutscher (ed), *Guide to Protein Purification, Methods in Enzymology*, Vol. 182 (1990). If the protein is secreted, it can be isolated from the supernatant in which the host cell is grown. If not secreted, the protein can be isolated from a lysate of the host cells.

The invention further provides transgenic plants capable of expressing an exogenous variant gene and/or having

one or both alleles of an endogenous variant gene inactivated. Plant regeneration from cultural protoplasts is described in Evans et al., "Protoplasts Isolation and Culture," *Handbook of Plant Cell Cultures* 1, 124-176 (MacMillan Publishing Co., New York, 1983); Davey, "Recent Developments in the Culture and Regeneration of Plant Protoplasts," *Protoplasts*, (1983) - pp. 12-29, (Birkhauser, Basal 1983); Dale, "Protoplast Culture and Plant Regeneration of Cereals and Other Recalcitrant Crops," *Protoplasts* (1983) - pp. 31-41, (Birkhauser, Basel 1983); Binding, "Regeneration of Plants," *Plant Protoplasts*, pp. 21-73, (CRC Press, Boca Raton, 1985). For example, a variant gene responsible for a disease-resistant phenotype can be introduced into the plant to simulate that phenotype. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer. Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. *See* Capecchi, *Science* 244, 1288-1292 (1989). Such transgenic plants are useful in a variety of screening assays. For example, the transgenic plant can then be treated with compounds of interest and the effect of those compounds on the disease resistance can be monitored. In another example, the transgenic plant can be exposed to a variety of environmental conditions to determine the effect of those conditions on the resistance to the disease.

In addition to substantially full-length polypeptides, the present invention includes biologically active fragments of the polypeptides, or analogs thereof, including organic molecules which simulate the interactions of the peptides. Biologically active fragments include any portion of the full-length polypeptide which confers a biological function on the variant gene product, including ligand binding, and antibody binding. Ligand binding includes binding by nucleic acids, proteins or polypeptides, small biologically active molecules, or large cellular structures.

Polyclonal and/or monoclonal antibodies that specifically bind to one allelic gene products but not to a

second allelic gene product are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide fragments thereof. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A Laboratory Manual*, Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of immunoreactivity to the corresponding prototypical gene product. These antibodies are useful in diagnostic assays for detection of the variant form, or as an active ingredient in a pharmaceutical composition.

V. Kits

The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10, 100 or all of the polymorphisms shown in Table 1 or 2. Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the methods.

EXAMPLES

As noted above, the sequences in Table 1 were isolated from *B. napus* and *B. oleracea* using oligonucleotide primers designed from expressed DNA sequences from *Arabidopsis thaliana*, a relative of *Brassica napus* and member of the

Cruciferae family. Primers used to amplify *B. napus* and *B. oleracea* alleles were selected for an optimal length of 20 bases ± 2 based such that their melting temperatures were between 60°C and 65°C. Primers were synthesized on a 20 nmole scale using a high throughput DNA synthesizer capable of producing 96 primers simultaneously in a 96-well format. See Lashkari et al., *Proc. Nat. Acad. Sci.* 92, 7912-7915 (1995). The primers, which have an average length of 21 bases, were positioned within DNA sequences such that PCR products produced with cDNA templates would range between 100 and 450 bp. As introns in *Arabidopsis* genes are of modest size, 60% of the 1,920 primers tested on plant DNA gave PCR products.

The components needed for PCR amplification were mixed in the following proportions for a 96 well microamp tray assembly: 206:1 of 10X PCR reaction buffer, 206:1 of 2 mM dNTPs, 186:1 of 15 mM $MgCl_2$, 720:1 of sterile ddH_20 and, 20:1 of Taq DNA polymerase (Perkin Elmer). The enzyme was added just prior to dispensing 168:1 of this master mix into 8 tubes. 20:1 of the appropriate forward and reverse primer 10 pmol/l stock solutions was added to each tube. A volume of 14:1 of this mixture was dispensed into each well of the microamp assembly with a BioHit 8-channel pipette. A volume of 5:1 of 20 ng/l template DNA solutions was added to the microamp assembly with a 12-channel pipette. The assembly was centrifuged for 30 sec to ensure that all reagents were mixed. Amplifications were performed in a Perkin Elmer system 9600 thermal cycler with an initial denaturation at 95°C for 1 min followed by 40 cycles of 94°C for 30 sec, 55°C for 30 sec, 72°C for 30 sec and a final extension at 72°C for 5 min. Products were separated by electrophoresis at 120 volts for 1 hr through 2% (w/v) agarose gels prestained with ethidium bromide. The banding patterns of these gels were recorded with an Alpha Innotech gel documentation system.

Any two amplicons obtained from the same primer set with two different plant varieties are said to be homomorphic if they have the same size. A set of 355 homomorphic *Brassica napus* and 250 homomorphic *Brassica oleracae* fragments were purified with Quiaquick columns and sequenced using dye

labeled dideoxy-terminators. See Stryer, *Biochemistry* 2nd. ed., pp. 592-593 (1981). The same primers used for the PCR amplification of the homomorphic DNA fragments were also used for the DNA sequencing of these fragments. The sequences obtained were aligned to identify single nucleotide polymorphisms.

Using VLSIPS™ technology (US 5,143,854; WO 90/15070; WO 92/10092), GeneChipJ was constructed using 20mer-probe sets to identify by hybridization the presence or absence of many of the polymorphisms shown in Table 1 in a sample of plant nucleic acid. The tiling strategy used to create the GeneChipJ is set forth in Figure 1. Tiling strategies can be devised using the guidance provided herein by those skilled in the art. Tiling arrays are described in PCT/US94/12305 (incorporated by reference in its entirety for all purposes). ATiling@ generally means the synthesis of a defined set of oligonucleotide probes that is made up of a sequence complementary to the sequence to be analyzed (the target sequence), as well as preselected variations of that sequence. The variations usually include substitution at one or more base positions with one or more nucleotides. Tiling strategies are discussed in Published PCT Application No. WO 95/11995 (incorporated by reference in its entirety for all purposes). In general, with a tiled array containing 4L probes one can query every position in a nucleotide containing L number of bases. A 4L tiled array, for example, contains L number of sets of 4 probes, i.e. 4L probes. Each set of 4 probes contains the perfect complement to a portion of the target sequence with a single substitution for each nucleotide at the same position in the probe. See also Chee, M., et. al., Science, October, 1996.

The tiling strategy for 20mer probes shown in Figure 1 for a single allele of the polymorphism employed probe sets having a perfect match and a corresponding single-base mismatch at the tenth base in the probe, counting from the 3= end. Each set had 14 pairs of probes that began at 14 successively shifted positions such that the substituted base lay from 7 bases upstream to 6 bases downstream from the

polymorphic site. Two such sets of 28 probes were included to query the polymorphic site for the two alleles, as shown for example, in Figure 1. This collection of 56 probes constituted a detection block. Two such blocks per marker were synthesized to query both the forward and reverse strands. Thus each marker interrogated by the GeneChipJ was represented by a full set of 112 probes.

All publications and patent applications cited above are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication or patent application were specifically and individually indicated to be so incorporated by reference. Although the present invention has been described in some detail by way of illustration and example for purposes of clarity and understanding, it will be apparent that certain changes and modifications may be practiced within the scope of the appended claims.

brassica1.list

Table 1

BRASSICA POLYMORPHIC MARKERS				
NUMBER	XMIN	YMIN	MARKER_NAME	SEQUENCE
1	0	3	85/5B5/86-1	AGCAAGCTTACATGCGTGGA[GT/AA]GAGAGTCCTCGAGATCAACC
2	33	3	85/5B12/N3-1	CCTTGATCTCTCAAGTAATC[A/G]TCTCACCGGAAGATCCCTGA
3	66	3	85/5C3/86-2	ACCATCCATTAAACTGTATC[A/G]TCGCAATCTAACCAAAAGTT
4	99	3	85/5E1/86-1	TAAAGCAAAGAGAGTCTTAC[C/A]GTCTGCTGCATGATATACCC
5	132	3	85/5E1/86-2	CTACTGATAGTGAACCACCC[A/C]ATCCCCAAATTTAAAGCAAA
6	165	3	85/6A11/86	ATCCTATTGGTAGTAACACA[G/A]ATTGAGTTAATGTTGCAGGG
7	198	3	N1/6A11/N2	AGGCAAAGCGGTAGTTGCAA[G/A]ACTGCTTCTCACGAGGTAAT
8	231	3	N1/6A9/N2-1	CCAGCTTCAATGTCTGCATG[C/A]TTGTGTCGATGCCAAAGTTC
9	0	11	N1/6A9/N2-2	AAAGTTCATTACGATGATCT[A/G]ACCCTGCAGTCATCCATGGA
10	33	11	85/6A12/86	CTTCCCCCCCCTCAATACCTC[T/G]TTCAAAAGTGAAAAGTGCAG
11	66	11	N1/6D1/N2-1	ATTTTGTTTTGTTTCTTGTC[G/C]GGTCAGGTCAGAACAAAGTT
12	99	11	N1/6H5/N2	AAACCAGAGCCACCTCCTTA[C/]CCACCTCATCGTTTCCTTTC
13	132	11	86/6F11/N2-2	GATTTCGACCGCAGTCTCAC[G/T]GAGGATGAGTATATCGCTTT
14	165	11	N1/6F11/N2	TAGGACAGGCAAACAATCTA[C/A]GCGGTCAAAATCCGATTTCG
15	198	11	L4/8A2/L6-2	AGCAGTGCAACAGCTCCTGC[A/T]AAGTCCCTGACGTACGAGGA
16	231	11	N1/8B5/N2	ACTCAAAAAAACGATACCTC[G/C]GCCGTCTCTCGCCGTCTCGC
17	0	19	N1/8D4/N2-1	CAGGAGACAGTTACAGTCCC[/A]CAGAGTCGCAAGGATCTCGAA
18	33	19	85/8D4/86-2	CTGATCTTGAAGGAGAGACC[A/G]CCACAAGGTTCCATCCTATG
19	66	19	85/8H11/86	AGTGCgAGGCTCAGTTGGAT[G/T]ATTAGGGTGTCAGTAAATCA
20	99	19	85/10B8/86	NAGGTCCATGATGATGACAA[T/A]AAAGGTATTCCACATGTCAA
21	132	19	N2/10B8/N3-2	ACATCCAACTTTTCTCCAGT[T/C]CTTTATTCTATCCTGATTTG
22	165	19	N2/10B8/N3-1	AAGGTATTCCATTGGTATAC[A/C]TCCAACTTTTCTCCAG[illegible]TCT
23	198	19	85/10B9/86	GACCTTCTTGGGAAAGAAAG[T/C]TGTAACCGCGTCGAGA[illegible]CG
24	231	19	L5/10C8/N2	ATAGAAACCGCCGATGCTCA[G/A]GGACACGCCACCGTCTTCGT
25	0	27	L6/10C8/N2	CACTTTCTTCGTGGCTAAAT[G/T]CTTCGGCCGAGCCGGTCTCA
26	33	27	L6/10D2/N1	GTTATCATCAGTACCGGTAT[C/T]AACCCCAAGGCTAATTCTTA
27	66	27	85/10D2/L6	TTGGGTATCTACGGACTGAT[C/T]ATCGCTGTTATCATCAGTAC
28	99	27	N1/10E12/N2-1	GGAATTCAATACTCGCCAAC[G/T]TCTTCATTGCTGTCGTCGGC
29	132	27	N1/10E12/N2-2	TCCTTACGCCTTCAAGCGCA[C/G]CGGCTGGCTCATGGGTGTCC
30	165	27	N1/10F4/N2	TGTATCTATGCGGTGGCTGC[G/C]GTCTCCGTTCGCGCCAGTAC
31	198	27	L1/10F4/N2*	GCGCCAGTACCGCCGGTTAC[C/A]ATCTcACTGCCTTCACGTCC
32	231	27	85/10F4/N2*	GCGCCAGTACCGCCGGTTAC[G/A]ATCTTAATGCCTTCACGTTC
33	0	35	85/10F9/N1-2	AACTTGGAATTCCACAACTT[G/C]AGAAACTTCGATGTGGTGCC
34	33	35	85/10F9/86	CGGTACTGCGAAAGCTGGAG[C/G]ATCAACTTGGAATTCCACAA
35	66	35	86/10F12/L3	AAAAGTGCTATTGTTCAGGT[G/C]GATGCTGCTCCGTTCAAGCA
36	99	35	85/10H6/86	GTCAAAAGCCACGGATTCAA[G/A]AACGTGCTCTTCTTGCGCCT
37	132	35	L1/10H6/L6	GCGGTGG[illegible]ACAGGCGCTCA[G/T]TTTCTCGTCAAAAGCCACGG
38	165	35	85/10F12/86	AAACCAGGGTCCTTGATGTG[T/]GTCTACAACGCTTCCAACAA
39	198	35	85/11B7/86	AANACCCTGAGCTCATGCCT[C/T]TGACCCATGTTCTTGCCACC
40	231	35	85/11C4/86	TTTGGGACCGTTGGAGTTGC[A/G]TCTGCGGCTATGACGGTGGA
41	0	43	85/11D4/86-2	AATCTTTGCCATTGCTGTCA[A/G]TATCTTCGTCAGCTTCAGCT
42	33	43	L4/11A3/L1	TTGAAGGAGGTTGGTACACA[C/G]TTCTTCGAGCTACCGGAGAC
43	66	43	N2/11D11/N3	GACAACGCTGGTGGTATTGC[C/T]GAAATGGCTGGAATGAGCCA
44	99	43	86/11D11/N3	GCTGCTCTAGGGATGCTCAG[C/T]ACCATCGCCACCGGTTTGGC

brassica1.list

45	132	43	85/11D11/86	ATGCTCAGCACCATCGCCAC[T/C]GGTTTgGCGATTGATGCTTA
46	165	43	N2/11E3/N8a	GAGAAAGTGCTTGTGGAGAT[C/T]TACAaGTCCATACTGATGGC
47	198	43	86/11E3/N2a	AATGCTTGTGGAGATtTACA[G/A]GTCCATACTGATGGCGCAGG
48	231	43	86/11E3/N2b	AATGCTTGTGGAGATcTACA[G/A]GTCCATACTGATGGCGCAGG
49	0	51	85/11F12/86	AATGATTGGTTTGAGAAGCA[T/A]ACAGCTGGTACGCTTGATAT
50	33	51	85/11F7/86	GATAGGGCGAAGAGAGGGAA[G/A]AGTCCTGAGAGGAAAGAGAT
51	66	51	85/11H2/86-2	CTCTCTCTCCACAAAGACAC[A/C]GCTTTCTCCATGACCTTCGG
52	99	51	85/11H5/86-2	TCTCTGACGTCATGAAAGCT[C/A]ATGGCAAAATTGCTGATGGA
53	132	51	85/11H6/86-1a	GTTATCGATCGCGTGGTCCG[T/C]GAAACCCAAAATaCACCTTT
54	165	51	85/11H6/86-1b	GTTATCGATCGCGTGGTCCG[T/C]GAAACCCAAAATtCACCTTT
55	198	51	85/12B6/N3	CGTCAGCCTTCTTCCGCCGC[A/C]GTCGTCCTCCGCAACCGTGC
56	231	51	86/12B6/85a	TGTCTCTTCCGTCAGCCTTC[C/T]TCCGCCGCAGTCGTCCTCCG
57	0	59	86/12B6/85b	TGTCTCTTCCGTCAGCCTTC[C/T]TCCGCCGCcGTCGTCCTCCG
58	33	59	86/12B11/85	TCAGGTTTACCTCTATATAT[T/]ATATTTCATGGTATGAAGGT
59	66	59	n1/12B11/N2-2	TATCCTGCAAATTGACATTT[T/C]CCTTCAGGTTCTAGAAGCTG
60	99	59	85/12C2/86	CGAGAACAGAAGAGAAGAGA[C/]TGGAACACGTCGGACAGTAC
61	132	59	L3/12C7/L5	TGNCACAACGAAGGTTTTGG[C/T]GGAGGTAAATGCCGTGGGTT
62	165	59	L6/12C11/N2	ACGGGTCCTAGCGCCATGGC[C/T]ATTTTCCTCACCGTTTCTGG
63	198	59	N1/12D10/L6	TTGGGCTTTCGGTGGTATGA[T/]CTTCGTCCTCGTCTATTGCA
64	231	59	L2/12E10/L3	CACAAAGGTCTGCCTCACAA[G/T]TTCTACCACGGTCGTACTGG
65	0	67	85/12F4/86-1	TCCTTGATTCCTTAATAATC[A/T]TTGGCTGGGGGTCTTTCTAA
66	33	67	L1/12G5/N1	GCTTGAATAACGATGTCTAC[A/T]CTGCCTCGGCGTACGGCGGA
67	66	67	85/12G8/L1	CTAAAAAGATCGACGAGTGT[C/T]CCTTACTACGCTCCATCTAT
68	99	67	L6/12G9/N1-1*	AGGTGGGTTTAGCGTGGCAT[T/C]CGATCCATTGGATGGATCCA
69	132	67	85/12G9/L3*	NGTGGGTTTACCGTATCATT[T/C]GATCCATTGGATGGATCGAG
70	165	67	L3/12B11/N2-1	GCGGATCCTATATTGGGTCT[C/T]GATGGATTGTTTCTATCCCG
71	198	67	L2/12B11/N2-2	TATCCTGCAAATTGACATTT[T/C]CCTTCAGGTTCTAGAAGCTG
72	231	67	N1/12E10/L1	TACCACGGTCGTACTGGTCG[A/]TGTCTGGAACGTCACCAAGC
73	0	75	N1/13A3/N2a	CTGTCTCAgTTTGTTGGATC[C/G]AAATCgAATCGAAAGCGTAC
74	33	75	N1/13A3/N2b	CTGTCTCAgTTTGTTGGATC[C/G]AAATCaAATCGAAAGCGTAC
75	66	75	L2/13E8/N2	ACACTGTTGGAGGACGTGAA[T/G]AAGATATTCAAGACAACATC
76	99	75	N1/13F6/N2-2	TCTTTCGTATCTTGCTGAGT[C/T]GTTACGCCTGTCAACACCCG
77	132	75	L2/13F8/N2-1	GGAACCCTAGGGAGCCCACA[T/G]CTCCTTATGCTAAGCGGCGT
78	165	75	L3/13F8/N2	GATCATAGTATCCGCCGGAA[G/C]CCTAGGGAGCCCACAGCTCC
79	198	75	85/14B5/86	TTCGGCGGGTCGATCCGGGC[A/G]GAAGACATTGTCAGGTGANN
80	231	75	N1/14C2/N2*	GCACCAACATTGTAAACCTA[T/G]AGCTTCTTCCTCAGCCACCT
81	0	83	85/14C2/86-1*	GCTGCCACATAGTGAACCTA[T/A]AGCTTCTTCCTCAGCCACCT
82	33	83	N2/14C2/85-2*	GCACCAACATTGTGAACCTA[G/A]AGCTTCTTCCTCAGCCACCT
83	66	83	85/14C2/86-2	AGTACATAGCTATTGACTAA[C/G]TTAAGTTCCTTGTATTGTTG
84	99	83	N2/14C2/85-1	CCTCTATCCGCCATGGTTGC[A/T]CCAACATTGTGAACCTAGAG
85	132	83	85/14E2/86-2	TTGACCCTCGGCAAGCCACC[G/T]GTCAAGCCATGCTGCAGCCT
86	165	83	85/14E2/86-1	AGGCTGCCCTCTCCCAATTC[A/C]AAAGCCAACTCCTAAACCAA
87	198	83	85/14E8/86	AAACATGGAAAGGCCTGATA[/G]TCACCGTCAAGCTCACCGTC
88	231	83	85/14E12/86	CAACCTGAAAAATTGTTTTA[C/A]CAACGGCCCCGCTTTCTCCA
89	0	91	L1/14H10/86	AAGGCCAACAACGACATTAC[T/C]TCCATCGTTAGCAACGGAGG
90	33	91	85/14H10/86	TCACCGGCTTGAAGTCTTCC[G/T]CTGCATTCCCAGTCACCCGC

brassica1.list

91	66	91	85/15A6/86	ACTCAGCTTTCTTATGCCTC[G/]ACTTGCGACACACGAATCCA
92	99	91	85/15C4/86	TGCGGCTAACATCTCTGGTG[G/T]TCACCTTAACCCAGCCGTAN
93	132	91	85/15E5/86-1	CGAGGATCACTTCTCTCTGT[G/T]CAAGAAGAAGTTCGGcAAGG
94	165	91	N1/15E5/N2-1	CTGTtCAAGAAGAAGTTCGG[C/T]AAGGTCTACGCTTCCCGCGA
95	198	91	N1/15E5/N2-2	CCCTCTGCTCGTCACGGCGT[T/A]ACGCAGTTCTCGGATCTGAC
96	231	91	86/15E5/N2	CCCGCGAGGAGCACGACTAC[A/T]GATTCTCCGTTTTCAAATCC
97	0	99	L1/15E9/86*	TCCACTCGCCGGGAAGAAAC[A/T]CGACAAACCGTTGTCTACTT
98	33	99	N2/15E9/L1	ATGGCTCGCGACGGGTCTCC[G/T]GTAAACCTCGGAGAGCAGAT
99	66	99	N2/15E9/86	GCCGACTCTCGAAGCTTCTT[A/]ACTCCACTCGCCGGGAAGAA
100	99	99	85/15E9/86-1	GAATCTAGGAGAGCAGATCT[T/G]CCTCTCTATCTTCAATGTTC
101	132	99	85/15E9/86-2*	TCCACTCGCCGGGAAGAAAC[C/T]CGACAAACCGTTGTCTACAT
102	165	99	N1/15E9/N2-1	GTCATGAAGATATTCACTAC[A/G]CCGACTCTCGAAGCTTCTTA
103	198	99	85/15F1/86	GCAGGTAAAATTCTACAGAC[C/A]TTCCCTTTTCATTGTAGTTA
104	231	99	85/15F5/86	TCTCCTCCGCCGCGCAAGAA[G/A]AAATCGACAGCGGCGCGTCT
105	0	107	85/15F10/86	GTGCCCTAAAGATACCCTCA[A/G]GCTTGGTGTCTGCGCTAATG
106	33	107	N2/15G1/L3	TTCTTCCCACAGGTGAAACT[T/C]GCTAACTTCCTTCCAAAGTA
107	66	107	N1/15H7/N2	TATGTATCAGGACAATGTGT[GA/TT]GTGACTGTGGTTGCATCCAT
108	99	107	N1/16A1/N2-1	GCTAAGCTACGCAACTGCCA[C/T]CAATCAGGGCAAGCTAAAGG
109	132	107	85/16A5/86	TATACACTCTTTAAAAGCGT[G/C]TGTGTGTACCCATCTCTCTT
110	165	107	N1/16B6/N2	ATGGCTGCGTATTGGCTGTC[C/T]AAGGCTGGATCTTGGTCCCA
111	198	107	85/16B6/N1	GGATCCATCTCAACTATGGT[A/C]GTATTATCGTTGAGGCTAGG
112	231	107	85/16B7/86	GTATGTGATTCGGAAGAGAA[T/]CAAACTAAGTGCCGAGAAAG
113	0	115	N1/16D6/N2	GCTAAGGTAGTTGGAGGAGC[CAA/GTG]CCACAGCCACGCGACTAAGG
114	33	115	85/16D10/86	CTCAACGTAGCAAGTAATAA[T/G]ATACTGTCTATTTATGGTTA
115	66	115	N1/16E9/N2	AGACTTTCCCCATTCTCTTC[T/A]CCATCCACCGTCGAAACCCA
116	99	115	85/16H3/86-1	ACTTCGAAACTGTAAACCTA[A/T]ACTTTAAGAGTTTAGAGCTA
117	132	115	85/16H3/86-2	CACCATCGGAGAAAGAGGTA[C/T]TTCGAAACTGTAAACCTAAA
118	165	115	85/17A5/86	CTAAGGCGTCTCCTGAAGAA[A/G]TACAGAGAGTCGAAGAAGAT
119	198	115	85/17C7/86	CCGCGGACGACGCTTTCTTC[C/A]TCTGCTCCACCGCGAGCGCC
120	231	115	85/17F7/86	GAGGAGTAGTCTCCATGGCC[G/]AAGAAGAGCGTCGGAGACCTG
121	0	123	85/17G12/86	GAAGTTAGGGCTTCTAAGAT[C/T]AAGTTCGGCAAGGCTTTAAC
122	33	123	85/18A2/86	TCAAAACTAATATTTCTTTT[G/C]TTGATTGGTAATAAACAGGT
123	66	123	85/18A11/86	TTCCAGTGAAAAGGCATTGT[T/G]CTCCAAAATCTCGCTCTGCG
124	99	123	85/18F5/86	AAGCAGCTCTGACTTGAATG[C/A]GAGAGGTTAATCAGACTGTG
125	132	123	85/18H10/86-3	TAGATTGAAGCAATCAAGAA[G/A]ATCTCAGACTTCATCACCCA
126	165	123	85/19B3/86	GCATCCAACTCCAAGGATGA[/C]CCTGCCAAGGTGCTGCTAACT
127	198	123	85/19C8/86	GAGCTCAGGGATGGTGGATC[A/T]GACTACCTTGGAAAGGGTGT
128	231	123	N1/19F4/N2	TGGGGTTAGTCGAAATAGGT[A/T]AAATGCTTTGAGTATGTGTA
129	0	131	N1/19H1/N2	TACGCGCAGCACGGACTTGC[G/A]ACGCAAGCAATCGAGCTTTT
130	33	131	85/20B4/86-1	GAAGCCCATGGTACGGAGCG[G/A]GAGAGAGTCAAGTACTTGGG
131	66	131	N1/20B12/N2	AACGGGTCACTGCTAAATCA[T/A]AAGGATCACAAGGCTGGGAC
132	99	131	85/20C12/86	CTAGCCTACTTTGGGAAAAG[/T]TTCGTTATTGTTTTGTGTGG
133	132	131	85/20D2/86	GACTTCAAGGACTTCGCCGG[A/C]AAATGCTCCGACGCTGTCAA
134	165	131	85/20D3/86-2	GAGGAGGGCTACATGCAGCT[G/A]AAGAGGCTGAGGGGGCTAAA
135	198	131	85/20D6/86-4	GATGTTCAACCTATGAAGAA[G/C]AAACACCGAGGACCAACGAG
136	231	131	85/20D6/86-5	CCATTAGTGAGGGAGCATGT[T/A]CCTGTCACATTTGATGATTG

brassica1.list

137	0	139	B5/20D6/B6-8	AAACACATCGCCAAAGATCC[CG/AA]ACACTCGAGAAAGAGTGGAG
138	33	139	N1/20D8/N2	CTCATAGGCGATCTGGAGTA[T/G]GCAAATCGAATCTCCTCTCC
139	66	139	N1/20E1/N2	TGCACGCCTCACTTGTTCCT[T/A]CCAATCTGACATCAAGGATT
140	99	139	N1/20F1/N2-1	NGTGTTTTTGAGGTGAAAGC[A/T]ACAAATGGAGATACCTTTTT
141	132	139	N1/BoC-a2/N3-2	CCCGAGCCATTAGGACAAGA[T/C]GACTTGCCGTTTGACCAAAC
142	165	139	N1/BOC-A2/N3-1	CCCATCTCATCCTTTCTTGA[A/G]CCGTTGAATCAAGCTCCTGG
143	198	139	N1/BoC-a2/N3-3	TACATTCTCATTGGTTGGTT[C/A]TTGGGAAATAAAGTACCAAC
144	231	139	B6/SC3/L2	GCACGCGCTAGAGTTGTTGC[C/A]AGAAGGAATGAACAATCTGA
145	0	147	N3/SC3/N4-1	CTTGAGACCTATAGTCCTGT[A/T]GTTCGGTCCGCCACAGTTCG
146	33	147	N3/SC3/N5-1	CACAGTTCGTACAGTTCTTC[A/C]CATTGCCACTGTTATGCACT
147	66	147	N1/SC3/N3-1	GAAGGCGTCCACTATCTTGA[A/G]ACCTATAGTCCTGTTGTTCG
148	99	147	B6/SC3/N4-1	TCCCGGAAATCTTGCTGAAA[A/C]CGTTTACCTGCGACAACCAG
149	132	147	L3/B11/N5-1	ATGTCTTCAAAGTGCTCTGT[C/T]GCAACGCACGTCCGAACAAG
MAIZE POLYMORPHIC MARKERS				
NUMBER	XMIN	YMIN	MARKER_NAME	SEQUENCE
150	165	147	s71/g2/g6-1	ATAATACTTGATATGCCATT[G/T]TGTCCTCTTATTTTTAACAT
151	198	147	S67/G1/G3-3	GTACCTGCCGCCGCTGTCGA[CG/AC]GGACGACCTGCTGAAGCAGG
152	231	147	s67/g1/g5-1	ATGGCCTCGTCGGCCACTGC[A/C]GTCGCTCCGTTCCATGGGCT
153	0	155	S66/G1/G3-1	AATGTAATGGTACTCCGCGC[T/C]ATGGCTCTGGTACTTAGGAA
154	33	155	s65/g3/g6-2	ACCACTGACGTAGCACCTCC[G/T]ACTTCTCGTTGTAAAACCCC
155	66	155	S65/G3/G5-1	GGAGGTTCGCCTCATGTTAT[C/T]GTTGACGAGCCACATCCACT
156	99	155	S64/G1/g3-1	CTGGTTGAAATGTGTTGAAG[C/A]TACTAGTGATGAACTGCTTG
157	132	155	S63/g3/g6-1	TCTGTGATTGGAGTCTGCTC[G/A]CGTGTCAGCTCTGGATGTGA
158	165	155	S63/G4/G6-1	TACTGAGAGAATGCAACATC[C/G]AGCATTCTGTGATTGGAGTC
159	198	155	S57/G1/G2-4	GAAGCCAAATCCTATTATTT[T/C]CTGCCTCTAGGGTCTGAATG
160	231	155	S56/G4/G6-2	GCCTTATCATCCTCTAGGTA[T/A]TGGAGACGAGTGACCAGTCT
161	0	163	S56/G4/G6-1	GTACACTGTTACAATCACAC[T/G]TAGTGAAGCGCAACACAGAT
162	33	163	S53/G5/G6-5	GAGCGAGATCGATCCTGTTG[T/C]CATCCATCACTGCCATAGGA
163	66	163	S53/G4/G6-1	TAGTCATAGCAACAGCATGC[G/A]TCGTGATGTAGCGTTCACCC
164	99	163	S53/G1/G6-2	GAACAGAGTCCGCAATAGTT[T/C]ATCCTAATGCTACTTCGAGC
165	132	163	S53/G3/G5-1	CCCACGGCGGGAGATGGTGG[T/]TAGAAGCGGAACCACCGAGC
166	165	163	S49/G4/G5-1	CGGTGACCCGATGATTATGG[T/C]GGCGGCCACACCTGCAATGA
167	198	163	S49/G5/G1-2	CAAGCAAGCAAGCTGTCTGT[C/T]CGTATGTGTCTGGCATGTTA
168	231	163	S49/G2/G6-1	TGCTGCTGCACTTGCTCATC[G/C]TTACTGATTTGCTGAAATGT
169	0	171	S49/G6/G1-3	TTTGCGCGCAATAAATCAGA[A/G]AGCTGATCTGAATCTGACCC
170	33	171	S49/G3/G6-1	CCACCCCGTTGCAGTGCTGT[/T]GCTGCTGCACTTGCTCATCG
171	66	171	S48/G3/G6-1	GATTCAGAAACAGTGGCGGC[A/G]GATGTAGCATCAACACGCCC
172	99	171	S47/G1/G3-4	CTCCTCGTGGTAGTGACGAT[G/C]ATTGCATCGGTGCCACAGGC
173	132	171	S47/G1/G3-3	GGAATACTCGATAGGCTCCC[A/G]CTGTGGGTAACAGTATTCCT
174	165	171	S46/G1/G2-1	TTCGGTGTCACTGACCTGTA[G/A]CATCAGCAGTAGCAGCGCCC
175	198	171	S45/G4/G6-1	TCCGCGGAAACAACATCCGA[G/T]TTCTTGAGGATAACCCAGCT
176	231	171	S45/G5/G6-1	ATGAGTATATTCAAGTCATA[T/C]TGTGAACTAGAATGTTATTT
177	0	179	S44/G5/G6-1	GCTGCGTCAATCATCACTTC[T/A]CCCACAGGCGTCAAGTACAG
178	33	179	S44/G1/G6-1	GCGTCAAGTACAGATACGCA[A/G]CACGCCTCAGCTTCGCCTTG
179	66	179	S43/G2/G6-2	CTTGATTGCATTGCAGCTAC[A/G]AGAAGCCCGTGGAAGGCCGG

brassica1.list

180	99	179	S43/G2/G6-1	GCTGGTTCATTATCTGACCT[G/T]GATTGCATTGCAGCTACAAG
181	132	179	S43/G2/G3-1	CTGGTGGTGGTGCTTCTCTG[AAAC/]TGAAACTGAAACTGACTGCA
182	165	179	S43/G1/G6-1	TGAATGGTAACCCACAACTG[C/T]TCGCGTCCTGCTGGTTCATT
183	198	179	S43/G2/G4-1	TGCATGTGAACATTCATGAA[T/C]GGTAACCCACAACTGTTCGC
184	231	179	S43/G2/G5-1	TACCCGGAGCTGAACCTCCC[C/G]GAGAGATTCAAGTCGTCCTT
185	0	187	S43/G1/G5-1	GCCGACAGGGTCCTCACCGT[G/C]AGCCCCTACTACGCCGAAGA
186	33	187	S42/G5/G7-2	TCGCTGTCAGGGAGGGCGTC[T/G]TGCAGCTCGGCTCCATGAAA
187	66	187	S42/G2/G3-1	CTGCACTCCGATTGAGGGTC[C/G]GAAGCAGGGCAGCGCGTGTG
188	99	187	S42/G2/G7-1a	GTTCTCTGCACTCCGATTGA[G/A]GGTCcGAAGCAGGGCAGCGC
189	132	187	S42/G2/G7-1b	GTTCTCTGCACTCCGATTGA[G/A]GGTCgGAAGCAGGGCAGCGC
190	165	187	S41/G3/G1-1	CGCCAGATGAACCAGCTCAC[TA/AGT]ATCCTGCAAGAGATATCCCT
191	198	187	S41/G2/G5-1	GATAGCCACATAGAACCTAT[G/T]CCTCCAGCTAACAACACGAG
192	231	187	S40/G4/G2-1	AAGTACATGACACCTCCGGA[G/A]ATACGGCCAAGAATCCCGCA
193	0	195	S40/G1/G4-2	GGAGCTTAACGATACCAATC[GA/CG]AAATTCCCTCGCCGGGCAC
194	33	195	S38/G5/G7-2	ATAATGATGGAACCATGACT[G/A]CCGAAGATGAACCAACCTTG
195	66	195	S38/G5/G7-1	GAGATATATGGTACTTCTAG[G/T]AGATTCAAAGACATGGAGCA
196	99	195	S37/G6/G2-1	GGTCAATAAGATAACTACAC[C/A]AAACTCTGCGTACAGTCTCG
197	132	195	S37/G2/G3-2	TGCAGGCGGCAGCCGAAGCG[/A]ATCGAAGGCCTGACCGGTCT
198	165	195	S37/G4/G5-1	ATCGATGGACAAGGGAGGGT[A/G]ATCTCGGGGTGTGCCAGAGG
199	198	195	S37/G1/G6-3	CAATACGATCAGCCAGACAG[C/T]CACTGTGCAACATCAGCAAA
200	231	195	S37/G1/G6-2	AATTCAGCTCAAATCATAGG[T/G]CAATAAGATAACTACACCAA
201	0	203	S37/G2/G4-4	GTCTCCCGGATCCAGAATCC[C/T]ACCGCGTTACATCGCCTTTC
202	33	203	S36/G3/G6	TCACTTTTTAGTGGTGTTTA[C/G]ACTAAGGATGCTGACATTCT
203	66	203	S35/G2/G3-2	GCTCGAACTTCTAGTTGATT[A/G]CATGATTGCTATTACTGTTG
204	99	203	S35/G3/G6-1	TCTGAGATACATTCATTTAA[C/A]ATGTCAGATAAAGAAAACTC
205	132	203	S35/G4/G5-1	GGTTCGCACCATATCATGAT[C/T]GGAATGCCGCCTCAAAATGG
206	165	203	S34/G3/G5-2	GATTTTGTAGGTTGATGCAT[C/T]GTTTGATCTTTCTTATCTCC
207	198	203	S34/G2/G5-1	TGTAGGACTTGGAGAGCTTG[A/G]TAATTTACACATGCCTCTGT
208	231	203	S33/G4R/G6*	GGCAGACAACAGACAGATCA[AG/CA]CATGCTTGCATTTACTCTCA
209	0	211	S33/G4r/G2*	GGCAGACAACAGACAGATCA[A/C]gCATGCTTGCATTTACTCTCA
210	33	211	S33/G5/G6-2	TCAAAGTGGTGCAATCGCAA[T/C]CCACTTGGGCTTGCCGTGGT
211	66	211	S33/G2R/G3-1	ACGCATGCTTGCATTTACTC[C/T]CAGTCAAACTCAGTCCCGAA
212	99	211	S32/G3/G5-3	GAATCCACCATTCTTCCGAA[A/G]CTGCTTCCTACAAAACTCGA
213	132	211	S32/G3/G5-2	ATGAATTGAAGCTCTGAATA[C/T]AGAATCCACCATTCTTCCGA
214	165	211	S31/G3/G5-1	CAATGTCTTGTTCGTTATCA[A/G]CGAAAGTTTGAATCCCCACA
215	198	211	S31/G3/G4-1	TGTATCGGCTAGTCTGGATG[G/A]TCGCACTGGCACTCAGTGCT
216	231	211	S29/G4/G5-1	TCTATTCAGCAGTCTGAGAA[GCA/CT]AGGATGGTCGGCTTCTTCAG
217	0	219	S29/G1/G5-1	CCTTACACTATTAACAGGCC[C/T]GTGATCTACCTGAATGCCTG
218	33	219	S28/G2/G6-1	GAATGTTGCTGTTATATTAC[T/C]CGTAGGTGACAAAGGGTTCA
219	66	219	S28/G3/G6-1	GTCGTAGCTTCCTCAAGACC[T/]TCCTGATGTGCGGACGCTAA
220	99	219	S28/G3/G4-2	AGGGGGTGGTCGCGACTGGA[T/G]CGCCCGAGCAGCGAGCAAGC
221	132	219	S28/G1/G3-1	TACATCTTAACAAGCACATG[TG/TTT]TAACCTTTTATTCAAACTTT
222	165	219	S28/G5/G6-1	CAAGAAGCCTCTTCAGTGTC[A/C]GTCGTAGCTTCCTCAAGACC
223	198	219	S27/G3/G6-2	TTCGCTTGGTAGCCGTAGCA[G/A]TATACTTTTACCGGCCACAG
224	231	219	S26/G5/G6-1	CCAAGAAAGATTAATGCTGG[/T]TAAAATATTGTTTCCAGTCT
225	0	227	S26/G4/G5-2	ATGCTGGTAAAATATTGTTT[/C]CAGTCTTTCACAAAGTGTGT

brassica1.list

226	33	227	S23/G5/G3-1	TTAAGTGAAGATGCCCAAAC[C/G]GTTAAACTTTCCATGGAACT
227	66	227	S23/G1/G5-1	CGGGTCTGTATGCGAGTGTT[G/A]TGGTGGTGAACTGGTGAATT
228	99	227	S23/G4/G5-2	TTCCAGTCGGATGAACTGGA[T/G]GTTCGTCATCCACTCGTCAC
229	132	227	S22/G5/G6-1	CAGATTGGTGTCGTTTACTA[A/G]AATTCAGTTCTGTCCATTTG
230	165	227	S21/G2/G5-1	TGGCTTGGTTGACCTTGAGG[C/G]CCACACACTATCTAGTACGT
231	198	227	S20/G5/G6-1	GCCGCCGAGAGCGAGGCATA[G/T]GCGCATGTGCATGTGCGTGC
232	231	227	S19/G5/G6-2	AGTACATGGCGAGCGTTGTA[G/C]CAGCTGCTTAGGTGATGTGG
233	0	235	S17/G3/G6-1	GGTTCTAAACATAGCTCGTC[C/A]ATTCATGATTCATCTCGAGC
234	33	235	S17/G4/G6-1	CTATTTCCaAGCTAACAACC[C/G]CTCTTGGTCCCAACATCCTG
235	66	235	S17/G3/G7-3	AAGCCTCATGTGCAGATTCA[TC/AG]GAACACACAACGTCAGCCAT
236	99	235	S16/G1/G2-1	GTGTGTAGCTTCATTCGCAA[A/T]GTTTGAACAGCCTCTGCAAG
237	132	235	S16/G4/G6-1	TCAGCAAGCCTCCAAGGCTC[C/A]AATGGTCCAGTTACTTGGTT
238	165	235	S16/G2/G7-2	GTTGACCAGCTGTGATTTCG[G/A]TGTATTCCACGACCACGAGT
239	198	235	S16/G1/G7-1b	CTTAATTGTACACAGTGCTT[C/T]CGTAAACCTAGAGctGACCA
240	231	235	S16/G1/G7-1c	CTTAATTGTACACAGTGCTT[C/T]CGTAAACCTAGAGtgGACCA
241	0	243	S16/G6/G7-1a*	GTGCTtcCGTAAACCTAGAG[TT/CT]GACCAGCTGTGATTTCGATG
242	33	243	S16/G6/G7-1b*	GTGCTTTCGTAAACCTAGAG[CT/TG]GACCAGCTGTGATTTCGATG
243	66	243	S14/G5/G7-2	CGAAAGAGCGAGATATATCG[A/G]TCGATCGATGAGCAAGTATA
244	99	243	S14/G5/G6-1	GCTCAGCTGCCGGAGTACGT[A/T]GGCTTGCTCTCCGGCCGGCC
245	132	243	S13/G2/G6-1	TTGGTAATTTCAGAGCTAGA[C/G]AACTTACTGTGGTACACGCC
246	165	243	S13/G5/G6-1	TTTCACAACTCAACTGATTG[A/T]CTTGCTTTGATGTGGATTCT
247	198	243	S12/G2/G5-3a	CGTAATTACTTTGTTACtaC[TA/C]AGTAATTTTATATATATCCT
248	231	243	S12/G2/G5-3b	CGTAATTACTTTGTTACacC[TA/C]AGTAATTTTATATATATCCT
249	0	251	S12/G1/G5-3	CTTTACTGATTGGGTTACAA[A/G]AGGTTATTTCTTATTCAGGC
250	33	251	S12/G2/G4-3a	ATCCGTAATTACTTTGTTAC[TA/AC]CtaAGTAATTTTATATATAT
251	66	251	S10/G4/G6-2	AATTTGGGAAAATCAATGCA[GAA/CAC]ATCAGTGATTAATCCACATA
252	99	251	S10/G4/G6-1	AGCGACAGGGATGTCGAGCA[G/T]CTACGGAAGGCAATAATGAG
253	132	251	S08/G3/G6-1*	GCACGTCGTTGGTGAAGAAG[AC/CA]GCGGTACGGGTGCTTGTCGA
254	165	251	S08/G1/G4-1*	GCACGTCGTTGGTGAAGAAG[A/C]AGCGGTACGGGTGCTTGTCG
255	198	251	S08/G3/G5-1	AGGTACACGGGGAAGTCGGA[G/T]TGGTTCTTCACCACCACCGC
256	231	251	S08/G5/G6-1	GTCCCAGATCAGGTCCACGT[T/C]CGAGCTCGCTGTTCCCGCTT
257	0	259	S06/G2/G3-2	ACGGTGAGGAGTGGCACATG[A/C]GATGGAAAGTTCCTGTAGAC
258	33	259	S06/G2/G3-1	NAACCAAACCCTGACTATTA[T/C]AGGTAGATTAGACTAGACAC
259	66	259	S03/G2/G6-1	ATATCCATGTTGTCGCCTGC[/TG]TGTGCGCTTGCTTGCCGCTA
260	99	259	S02/G2/G5-2	GTGTGGAATGACCATCTCGT[G/C]GTGATGCCAGCATGCTGTTA
261	132	259	S02/G3/G7-1b	CAACGTGCAATAATAGAACA[T/G]GTGGTGTTTGTTAaGAAAGA
262	165	259	S02/G6/G7-1	CACGGCAGTTGGCAGTGTGG[A/]AAGGACTATCTCGTGGTGAT
263	198	259	S01/G4/G7-3	GCTAGAGCAAGAGTCAACAC[G/A]CGCGCGCATCACGCATGCCA
264	231	259	S01/G3/G7-2	AGCCAGGTTCTAACAGCTAG[C/A]GCAAGAGTCAACACGCGCGC

Table 2 bl0702.oldlist

marker	sequence
B6-5B5-N3	CTTACATGCGTGGAAAGAGA[G/]TCCTCGAGATCAACCCACGA
B5-5B5-N3	GATGCTAAAAAGCAAGCTTA[C/T]ATGCGTGGAGTGAGAGTCCT
B5-5B5-B6-1	AGCAAGCTTACATGCGTGGA[GT/AA]GAGAGTCCTCGAGATCAACC
B5-5B5-B6-2	CAAACTCTCTCAGATGCTAA[A/G]AAGCAAGCTTACATGCGTGG
B5-5B12-N3-1	CCTTGATCTCTCAAGTAATC[A/G]TCTCACCGGAAGATCCCTGA
B5-5B12-N3-2	TCTCGATCTGACATCTCTCA[A/T]CGTCCTTGATCTCTCAAGTA
B6-5C3-B5-1A	TCGTCGCAATCTAACCAAAA[C/G]TTAAAAACGCTAACGGTGTG
B6-5C3-B5-1B	TCGTCGCAATCTAACCAAAA[C/G]TTAAAAACGCTAACAGTGTG
B6-5C3-B5-1C	TCATCGCAATCTAACCAAAA[C/G]TTAAAAACGCTAACGGTGTG
B6-5C3-B5-1D	TCATCGCAATCTAACCAAAA[C/G]TTAAAAACGCTAACAGTGTG
B5-5C3-B6-2	ACCATCCATTAAACTGTATC[A/G]TCGCAATCTAACCAAAAGTT
B5-5E1-B6-1A	TAAAGCAAAGAGAGTCTTAC[C/A]GTCTGCTGCATGATGTACCC
B5-5E1-B6-1B	TAAAGCAAAGAGAGTCTTAC[C/A]GTCTGCTGCATGATATACCC
B5-5E1-B6-2	CTACTCATAGTGAACCACCC[A/C]ATCCCCAAATTTAAAGCAAA
B5-5E1-B6-3	AACTTTTCGATTTCAATATA[G/T]CAACTACTGATAGTGAACCA
B5-5E1-B6-4	TAACTCTACAACATTCACAA[C/G]CTGGGCCAACATATTTAAAC
B6-5E1-N3	GGGATATAGCAAANTTGAAC[A/C]ATATCAATTGTTGACGGAAC
L6-5H5-N1	CCAAATAGGTTCTGAGCCTT[C/T]ACTTTCTCCACCATCTCATT
L6-5H5-L4-1	CTCCACCATCTCATTGCTCA[T/A]TCCAGCAAAAAACATCTCTG
N1-5H5-L4-1A	CTCCACCATCTCATTGCTCA[G/A]TCCAGCAAAAAACATTTCGG
N1-5H5-L4-1B	CTCCACCATCTCATTGCTCA[G/A]TCCAGCAAAAAACATCTCGG
N1-5H5-L4-1C	CTCCACCATCTCATTGCTCA[G/A]TCCAGCAAAAAACATTTCTG
N1-5H5-L4-1D	CTCCACCATCTCATTGCTCA[G/A]TCCAGCAAAAAACATCTCTG
N1-5H5-L4-2	CCAAATAGGTTCTGAGCCTT[T/C]ACTTTCTCCACCATCTCATT
B5-6A11-B6	ATCCTATTGGTAGTAACACA[G/A]ATTGAGTTAATGTTGCAGGG
N1-6A11-N2	AGGCAAAGCGGTAGTTGCAA[G/A]ACTGCTTCTCACGAGGTAAT
L6-6A11-N2	TCCTCAGAGGCAAAGCGGTA[T/G]TTGCAAAACTGCTTCTCACG
B5-6A12-B6	CTTCCCCCCCCTCAATACCTC[T/G]TTCAAAAGTGAAAAGTGCAG
B6-6A12-N2	CCTGTAAAATCTTCTCTCTC[CT/TC]TACTTCCTTTCTCCCCCCCC
N1-6A12-N3-1A	TGTAAGATCCTCTCTCTCTC[CT/TA]TGTCAACTCTCCCCCCCCCC
N1-6A12-N3-1B	TGTAAAATCCTCTCTCTCTC[CT/TA]TGTCAACTCTCCCCCCCCCC
N1-6A12-N3-1C	TGTAAGATCCTCTCTCTCTC[CT/TA]TGTCAACTCTCCCCCCCCCT
N1-6A12-N3-1D	TGTAAAATCCTCTCTCTCTC[CT/TA]TGTCAACTCTCCCCCCCCCT
B5-6A12-B6-1A	TTTCAAAAGTGAAAAGTGCA[G/A]AAACTCATTTATTTATGTTT
B5-6A12-B6-1B	TTACAAAAGTGAAAAGTGCA[G/A]AAACTCATTTATTTATGTTT
B5-6A12-B6-1C	GTTCAAAAGTGAAAAGTGCA[G/A]AAACTCATTTATTTATGTTT
B5-6A12-B6-1C	GTACAAAAGTGAAAAGTGCA[G/A]AAACTCATTTATTTATGTTT
N1-6A9-N2-2A	AAAGTTCATTACGATGATCT[A/G]ACCCTGCAGTCATCCATGGA
N1-6A9-N2-2A	AAAGTTCATTACGATGATCT[A/G]ACCCTGCAGTCATCCATAGA
N1-6A9-N2-1A	CCAGCTTCAATGTCTGCATG[C/A]TTGTGTCGATGCCAAAGTTC
N1-6A9-N2-1B	ACCACTTCAATGTCTGCATG[C/A]TTGTGTCGATGCCAAAGTTC

← brassica start

bl0702.oldlist

N1/6D1/N2-1A	ATTTTGTTTTGTTTCTTGTC[G/C]GGTCAGGTCAGAACAAAGTT
N1/6D1/N2-1B	ATTTTGTTTTGTTTCTTGTC[G/C]GGTCAGGTCAGAACAAAGGT
N1-6F11-N2	TAGGACAGGCAAACAATCTA[C/A]GCGGTCAAAATCCGATTTCG
86-6F11-N2-1	GAGGATGAGTATATCGCTTT[A/G]TGTCTCATGCTTCTTGCTCG
86-6F11-N2-2	GATTTCGACCGCAGTCTCAC[G/T]GAGGATGAGTATATCGCTTT
N1-6H5-N2	AAACCAGAGCCACCTCCTTA[C/]CCACCTCATCGTTTCCTTTC
L4-8A2-L6-1	ACCGAAACCAATCTCCCAAG[T/]AAAGCTTATTCAGGAGCTTC
L4-8A2-L6-2	AGCAGTGCAACAGCTCCTGC[A/T]AAGTCCCTGACGTACGAGGA
L4-8A2-L6-3	AGCTTCAATGGCGGATGGGC[T/C]CTTCTAACCTCTGTTCTAAG
N1/8B5/N2	ACTCAAAAAAACGATACCTC[G/C]GCCGTCTCTCGCCGTCTCGC
85-8B5-86-1	AAACACTAAGTGTCNCTCTC[T/C]AAACTAGTGTGCAAAGCTCA
N1/8D4/N2-1A	CAGGAGACAGTTACAGTCCC[/A]CAGAGTCGCAAGGATCTCGAA
N1/8D4/N2-1B	CAGGAGACAGTTACAGTCCC[/A]CAGAGTCGCAAGGACTCGAAC
86/8D4/N1-1	ATCTCGAACTTCACATCTGC[G/A]TTGAGTTCTGCTGAGAGGCT
85-8D4-86-1A	AGTTACAGTCCCACAGAGTC[T/G]CAAGGATCTCGAACTTCACT
85-8D4-86-1B	AGTTACAGTCCCACAGAGTC[T/G]CAAGGATCTCGAACTTCACA
85-8D4-86-2	CTGATCTTGAAGGAGAGACC[A/G]CCACAAGGTTCCATCCTATG
85/8H11/86	AGTGCNAGGCTCAGTTGGAT[G/T]ATTAGGGTGTCAGTAAATCA
N2/10B8/N3-1A	AAGGTATTCCATTGGTATAC[A/C]TCCAACTTTTCTCCAGTTCT
N2/10B8/N3-1B	AAGGTATTCCATTGGTATAC[A/C]TCCAACTTTTCTCCAGTCCT
N2/10B8/N3-2A	ACATCCAACTTTTCTCCAGT[T/C]CTTTATTCTATCCTGATTTG
N2/10B8/N3-2B	ACCTCCAACTTTTCTCCAGT[T/C]CTTTATTCTATCCTGATTTG
85-10B8-86	NAGGTCCATGATGATGACAA[T/A]AAAGGTATTCCACATGTCAA
85-10B9-86	GACCTTCTTGGGAAAGAAAG[T/C]TGTAACCGCGTCGAGATTCG
N2/10B9/N3A	CAGATCGGTACTTTCAACCA[G/T]TCTCCTTCTCTGTCTCCACT
N2/10B9/N3B	AGATCCGGTACTTTCAACCA[G/T]TCTCCTTCTCTGTCTCCACT
N2/10B9/N3C	AGAGTCGGTACTTTCAACCA[G/T]TCTCCTTCTCTGTCTCCACT
N2/10B9/N3D	CAGACCGGTACTTTCAACCA[G/T]TCTCCTTCTCTGTCTCCACT
86/10B9/N3	TATTCAACCAGTCTCCTTCT[T/C]TGTCTCCACTATGTCGTTAG
85/10B9/N3	ACTGAGTTTGGTCTGTCTCT[A/G]TGTGTGTGTGTGTTGTAGTA
L6-10C8-N2	CACTTTCTTCGTGGCTAAAT[G/T]CTTCGGCCGAGCCGGTCTCA
L5-10C8-N2	ATAGAAACCGCCGATGCTCA[G/A]GGACACGCCACCGTCTTCGT
L6-10D2-N1	GTTATCATCAGTACCGGTAT[C/T]AACCCCAAGGCTAATTCTTA
L5-10D2-N2	GTGTTGGGTATCTACGGACT[C/G]ATCATCGCTGTTATCATCAG
85-10D2-L6	TTGGGTATCTACGGACTGAT[C/T]ATCGCTGTTATCATCAGTAC
85-10D2-L6	TAGGGTATCTACGGACTGAT[C/T]ATCGCTGTTATCATCAGTAC
N1/10E12/N2-1	GGAATTCAATACTCGCCAAC[G/T]TCTTCATTGCTGTCGTCGGC

bl0702.oldlist

N1/10E12/N2-2	TCCTTACGCCTTCAAGCGCA[C/G]CGGCTGGCTCATGGGTGTCC
N1/10F4/N2	TGTATCTATGCGGTGGCTGC[G/C]GTCTCCGTTCGCGCCAGTAC
L3-10F4-L6	CCGTCTCCGTTCGCGCCACT[G/A]CCGCCGGTTACCATCTCACT
L2-10F4-L6A	GTTACAATCTCACTGCCTCC[A/T]CCTCCGCTCCTATCGAGGAA
L2-10F4-L6B	GTTACCATCTCACTGCCTCC[A/T]CCTCCGCTCCTATCGAGGAA
L1/10F4/N2	GCGCCAGTACCGCCGGTTAC[C/A]ATCTTACTGCCTTCACGTCC
L1/10F4/N1-1	CTGACTCGTGCGGTGGCTGC[C/G]GTCTCCGTTCGCGCCAGTAC
L1/10F4/N1-2	CCTCCACGTCCGCTCCTATC[G/A]AGGAATCGATCGTGTCTCAC
85/10F4/N2	GCGCCAGTACCGCCGGTTAC[G/A]ATCTTAATGCCTTCACGTTC
N1-10F4-L4	GATATGATCACTTCCGCTGA[A/G]ACAGATGTTGTCGTCGTTGG
85/10F9/N2-1	CGGTACTGCGAAAGCTGGAG[C/G]ATCAACTTGGAATTCCACAA
85/10F9/L3-1	CGGTACTGCGAAAGCTGGAG[C/G]ATCAACTTGGAATTCCACAT
85-10F9-N1-1	ACGGTATTGTTTCTTCAGGG[T/G]TCTCGACAAACCTGAAACGG
L5-10F9-N2	GATCAACTTGGAATTCCACA[T/A]CTTCAGAAACTTCGATGTGG
L1-10F9-L4A	CAAACCTGAAACGGTACTGC[G/A]AAAGCTGGAGGATCAACTTG
L1-10F9-L4B	CAAACCTGAAACGGTACTGC[G/A]AAAGCTGGAGGATCAAGTTG
85/10F9/N1-2	AACTTGGAATTCCACAACTT[G/C]AGAAACTTCGATGTGGTGCC
L2-10F9-L4	TCAGGGGTCTCGACAAACCT[A/G]AAACGGTACTGCAAAAGCTG
L3-10F9-L4-1A	TGCGAAAGCTGGAGGATCAA[C/G]TTGGAATTCCACATCGTCAG
L3-10F9-L4-1B	TGCAAAAGCTGGAGGATCAA[C/G]TTGGAATTCCACATCGTCAG
L5-10F9-L6	TCAACTTGGAATTCCACATC[T/G]TCAGAAACTTCGATGTGGTG
85/10F9/L1-1	CAATTGCGGATGTCTTCATC[G/A]TCAACCCAAAACGGTATTGT
86-10F12-L3	AAAAGTGCTATTGTTCAGGT[G/C]GATGCTGCTCCGTTCAAGCA
85-10F12-86	AAACCAGGGTCCTTGATGTG[T/]GTCTACAACGCTTCCAACAA
L1-10H6-L6	GCGGTGGTAACAGGCGCTCA[G/T]TTTCTCGTCAAAAGCCACGG
85-10H6-L6	TTTCTCGTCAAAAGCCACGG[A/G]TTCAAGAACGTGCTCTTCTT
85-10H6-86	GTCAAAAGCCACGGATTCAA[G/A]AACGTGCTCTTCTTGCGCCT
L4-11A3-L1	TTGAAGGAGGTTGGTACACA[C/G]TTCTTCGAGCTACCGGAGAC
85-11B7-86	AANACCCTGAGCTCATGCCT[C/T]TGACCCATGTTCTTGCCACC
85-11C4-86	TTTGGGACCGTTGGAGTTGC[A/G]TCTGCGGCTATGACGGTGGA
85-11D4-86-1	GTTGTGGTAGCGACTGCGGG[G/A]CAGAGCCGGTGCGAGCCTGG
85-11D4-86-2	AATCTTTGCCATTGCTGTCA[A/G]TATCTTCGTCAGCTTCAGCT
85-11D11-86	ATGCTCAGCACCATCGCCAC[T/C]GGTTTGGCGATTGATGCTTA
N2-11D11-N3	GACAACGCTGGTGGTATTGC[C/T]GAAATGGCTGGAATGAGCCA
86-11D11-N3	GCTGCTCTAGGGATGCTCAG[C/T]ACCATCGCCACCGGTTTGGC
N2-11E3-N8	GAGAAAGTGCTTGTGGAGAT[C/T]TACAAGTCCATACTGATGGC
86-11E3-N2A	AATGCTTGTGGAGATTTACA[G/A]GTCCATACTGATGGCGCAGG
86-11E3-N2B	AGTGCTTGTGGAGATTTACA[G/A]GTCCATACTGATGGCGCAGG

bl0702.oldlist

N1/11F12/N3	TGGTTCTTTGGTGGGTTGCA[A/G]TTTCAGCTAGAGCATCATCT
85-11F12-86	AATGATTGGTTTGAGAAGCA[T/A]ACAGCTGGTACGCTTGATAT
85-11F7-86	GATAGGGCGAAGAGAGGGAA[G/A]AGTCCTGAGAGGAAAGAGAT
85-11H2-86-1	GGAGAAACCCTCTCCGACTT[C/T]CTCTCTCTCCACAAAGACAC
85-11H2-86-2	CTCTCTCTCCACAAAGACAC[A/C]GCTTTCTCCATGACCTTCGG
85-11H5-86-1	TCTCTGACGTCATGAAAGCT[C/A]ATGGCAAAATTGCTGATGGA
85-11H6-86-1	GTTATCGATCGCGTGGTCCG[T/C]GAAACCCAAAATNCACCTTT
85/12B6/N3	CGTCAGCCTTCTTCCGCCGC[A/C]GTCGTCCTCCGCAACCGTGC
L3/12B11/N2-1	GCGGATCCTATATTGGGTCT[C/T]GATGGATTGTTTCTATCCCG
L3/12B11/N2-1B	GCGGATCCTATATTGGGTCT[C/T]GATGGATTGTTTCTATTCCG
L3/12B11/N2-2A	TCTCGATGGATTGTTTCTAT[C/T]CCGCAAATTGACATACTCCT
L3/12B11/N2-2B	TCTTGATGGATTGTTTCTAT[C/T]CCGCAAATTGACATACTCCT
L3/12B11/N2-2C	TCTCGATGGATTGTTTCTAT[C/T]CCGCAAATTGACATTTCCCT
L3/12B11/N2-2D	TCTTGATGGATTGTTTCTAT[C/T]CCGCAAATTGACATTTCCCT
L3/12B11/N2-3	TATTCATGGCAACAATCTGT[C/G]GCGGATCCTATATTGGGTCT
L2-12B11-N2-1	TATTCATGGCAAGAATCTGT[G/T]GCCGATCCTATATTGGGTCT
L2-12B11-N2-2	TATCCTGCAAATTGACATTT[T/C]CCTTCAGGTTCTAGAAGCTG
86-12B11-85	TCAGGTTTACCTCTATATAT[T/]ATATTTCATGGTATGAAGGT
86/12B6/N3	TGTCTCTTCCGTCAGCCTTC[C/T]TCCGCCGCAGTCGTCCTCCG
85-12B6-N3	CGTCAGCCTTCTTCCGCCGC[A/C]GTCGTCCTCCGCAACCGTGC
85-12C2-86	CGAGAACAGAAGAGAAGAGA[C/]TGGAACACGTCGGACAGTAC
L3-12C7-L5	TGNCACAACGAAGGTTTTGG[C/T]GGAGGTAAATGCCGTGGGTT
L6-12C11-N2	ACGGGTCCTAGCGCCATGGC[C/T]ATTTTCCTCACCGTTTCTGG
N1-12D10-L6	TTGGGCTTTCGGTGGTATGA[T/]CTTCGTCCTCGTCTATTGCA
N1,2,3/12E10/L1	TACCACGGTCGTACTGGTCG[A/]TGTCTGGAACGTCACCAAGC
L2-12E10-L3	CACAAAGGTCTGCCTCACAA[G/T]TTCTACCACGGTCGTACTGG
85-12F4-86-1	TCCTTGATTCCTTAATAATC[A/T]TTGGCTGGGGGTCTTTCTAA
85-12F4-86-2	TACTTCTTGAGGAAGCAGGT[G/C]AAAATTAACAAGAGCAATGG
85-12F4-L1A	TTCCTTAATAATCATTGGCT[G/T]GGGGTCTTTCTAACTATAAG
85-12F4-L1B	TTCCTTAATAATCATTGGCT[G/T]GGGGTCTTTCTAACTATAAA
L1-12G5-N1A	GCTTGAATAACGATGTCTAC[A/T]CTGCCTCGGCGTACGGCGGA
L1-12G5-N1B	GCTTGAATAACGATGTCTAC[A/T]CTGCCTCGGCGTACGGTGAT
85-12G8-86	AAAAGGGTACAANCTANTAA[T/G]TGATGACTCAACTTTCANTT
L3-12G8-L6	GCAAAGCTAAAAAAATCGAC[A/G]AGTGTTCCTTACTACGCTCC

bl0702.oldlist

85-12G8-L1	CTAAAAAGATCGACGAGTGT[C/T]CCTTACTACGCTCCATCTAT
L5-12G8-L6	ACTCGGAGCAAAGCTAAAAA[G/A]ATCGACGAGTGTTCCTTACT
85-12G9-L3	GGTGGGTTTACCGTATCATT[T/C]GATCCATTGGATGGATCGAG
L6-12G9-N1-1A	AGGTGGGTTTAGCGTGGCAT[T/C]CGATCCATTGGATGGATCCA
L6-12G9-N1-1B	AAGTGGGTTTAGCGTGGCAT[T/C]CGATCCATTGGATGGATCCA
L6-12G9-N1-1C	AGGTGGGTTTAGCGTGGCAT[T/C]CGATCCATTGGATGGATCGA
L6-12G9-N1-1D	AAGTGGGTTTAGCGTGGCAT[T/C]CGATCCATTGGATGGATCGA
L6-12G9-N1-2A	TTCGATCCATTGGATGGATC[C/G]AGCATTGTGGATACAAACTT
L6-12G9-N1-2B	TCCGATCCATTGGATGGATC[C/G]AGCATTGTGGATACAAACTT
85/12G9/L3-1	GATCCATTGGATGGATCGAG[T/C]ATTGTGGATACAAACTTCAC
85/12G9/L3-2	TTGGGGTTTGGCCTGGTGAC[C/A]ATTTAACCGGACTCACGGGA
N1/13A3/N2A	CTGTCTCAGTTTGTTGGATC[C/G]AAATCGAATCGAAAGCGTAC
N1/13A3/N2B	CTGTCTCATTTTGTTGGATC[C/G]AAATCGAATCGAAAGCGTAC
L4-13A3-L5	ATGGAAAGTATGAATCTTTA[G/C]TCCACCCATTGTTCGCATTT
L4-13A3-N2A	TTTGTCCTGGTTCTGTCTCA[G/T]TTTGTTGGATCGAAATCGAA
L4-13A3-N2B	TTTGTCCTGGTTCTGTCTCA[G/T]TTTGTTGGATCGAAATCAAA
L4-13B6-N2-1A	TCTGAATAGGTCTTGGGGTT[A/T]TGTAAATTGTGTTGCGGGTG
L4-13B6-N2-1B	TCTGAATAGGTCTTGGGGTT[A/T]TGTAAATTGTGTTGCGGGTT
L4-13B6-N2-2A	ATGTAAATTGTGTTGCGGGT[G/T]TCTGAAAAGGGATTGGCGTT
L4-13B6-N2-2B	TTGTAAATTGTGTTGCGGGT[G/T]TCTGAAAAGGGATTGGCGTT
L3-13B6-L2	CTCTTCTTAGTCAATCTGAG[A/]AAGCCTGACGTCTCCTACAA
L2-13E8-N2	ACACTGTTGGAGGACGTGAA[T/G]AAGATATTCAAGACAACATC
N1/13F6/N2-1A	TCGAGGAACTGGAGATGGAT[A/G]AGGTAAACCTTTTGTTTTAT
N1/13F6/N2-1A	TCGAGGAACTGGAGATGGAT[A/G]AGGTAAACCTTTTGCTTTAT
N1/13F6/N2-2	TCTTTCGTATCTTGCTGAGT[C/T]GTTACGCCTGTCAACACCCG
L3-13F8-N2	GATCATAGTATCCGCCGGAA[G/C]CCTAGGGAGCCCACAGCTCC
L2-13F8-N2-1	GGAACCCTAGGGAGCCCACA[T/G]CTCCTTATGCTAAGCGGCGT
L2-13F8-N2-2	TAAGCGGCGTCGGGCCATCA[T/G]CTCAACTACAGGCCCAAAAT
85/14B5/86	TTCGGCGGGTCGATCCGGGC[A/G]GAAGACATTGTCAGGTGANN
86-14B5-L3	ACCCCTTCTTTTAGACCCAA[A/G]ACTCGCTTCGGCGGGTCGAT
N1/14C2/N2	GCACCAACATTGTAAACCTA[T/G]AGCTTCTTCCTCAGCCACCT
N1-14C2-L2A	AGCTTCTTCCTCAGCCACCT[T/G]CAACGAGAGCTCCTGGAAAC
N1-14C2-L2B	ATCTTCTTCCTCAGCCACCT[T/G]CAACGAGAGCTCCTGGAAAC
N2-14C2-85-1A	CCTCTATCCGCCATGGTTGC[A/T]CCAACATTGTGAACCTAGAG
N2-14C2-85-1B	CCTCTATCCGCCATGGTTGC[A/T]CCAACATTGTGAACCTAAAG
N2-14C2-85-1C	CATCTATCCGCCATGGTTGC[A/T]CCAACATTGTGAACCTAGAG
N2-14C2-85-1D	CATCTATCCGCCATGGTTGC[A/T]CCAACATTGTGAACCTAAAG
N2-14C2-85-2A	GCACCAACATTGTGAACCTA[G/A]AGCTTCTTCCTCAGCCACCT
N2-14C2-85-2B	GCTCCAACATTGTGAACCTA[G/A]AGCTTCTTCCTCAGCCACCT
N2-14C2-85-2A	CGAGAGCTCCTGGAAACCCT[T/G]GGCCACAGGTTTGTTTCTAT
N2-14C2-85-2A	GAAGAGCTCCTGGAAACCCT[T/G]GGCCACAGGTTTGTTTCTAT

bl0702.oldlist

N2-14C2-86A	AGCTTCTTCCTCAGCCACCT[T/AA]CAACGAGAGCTCCTGGAAAC
N2-14C2-86B	AGCTTCTTCCTCAGCCACCT[T/AA]CAACGAGAGCTCCTGGAACC
85/14C2/86A	AGTACATAGCTATTGACTAA[C/G]TTAAGTTCCTTGTATTGTTG
85/14C2/86B	ATTAAATAGCTATTGACTAA[C/G]TTAAGTTCCTTGTATTGTTG
85/14C2/86C	AGTAACTAGCTATTGACTAA[C/G]TTAAGTTCCTTGTATTGTTG
85/14C2/86D	ATTAACTAGCTATTGACTAA[C/G]TTAAGTTCCTTGTATTGTTG
L1-14C2-85A	GAAGAGCTCCTGGAAACCCT[T/G]GGCCACAGGTTTGTTTCGGT
L1-14C2-85B	CGAGAGCTCCTGGAAACCCT[T/G]GGCCACAGGTTTGTTTCGGT
L1-14C2-85C	GAAGAGCTCCTGGAAACCCT[T/G]GGCCACAGGTTTGTTTCTGG
L1-14C2-85D	CGAGAGCTCCTGGAAACCCT[T/G]GGCCACAGGTTTGTTTCTGG
85/14E2/86-1	AGGCTGCCCTCTCCCAATTC[A/C]AAAGCCAACTCCTAAACCAA
85/14E2/86-2	TTGACCCTCGGCAAGCCACC[G/T]GTCAAGCCATGCTGCAGCCT
85-14E8-86A	AAACATGGAAAGGCCTGATA[/G]TCACCGTCAAGCTCACCGTC
85-14E8-86B	AAAGATGGAAAGGCCTGATA[/G]TCACCGTCAAGCTCACCGTC
85/14E12/86	CAACCTGAAAAATTGTTTTA[C/A]CAACGGCCCCGCTTTCTCCA
85/14H10/86	TCACCGGCTTGAAGTCTTCC[G/T]CTGCATTCCCAGTCACCCGC
L1-14H10-86	AAGGCCAACAACGACATTAC[T/C]TCCATCGTTAGCAACGGAGG
85/15A6/86	ACTCAGCTTTCTTATGCCTC[G/]ACTTGCGACACACGAATCCA
85-15C4-86	TGCGGCTAACATCTCTGGTG[G/T]TCACCTTAACCCAGCCGTAN
N1/15C10/N2A	ACGGTGAGATCTAACGGCGG[G/C]GATCCTTCAGTCCATAGTCG
N1/15C10/N2B	ACGGCGAGATCTAACGGCGG[G/C]GATCCTTCAGTCCATAGTCG
N1/15C10/N2C	TCGGTGAGATCTAACGGCGG[G/C]GATCCTTCAGTCCATAGTCG
N1/15C10/N2D	TCGGCGAGATCTAACGGCGG[G/C]GATCCTTCAGTCCATAGTCG
86-15E5-N2	CCCGCGAGGAGCACGACTAC[A/T]GATTCTCCGTTTTCAAATCC
N1/15E5/N2-1	CTGTTCAAGAAGAAGTTCGG[C/T]AAGGTCTACGCTTCCCGCGA
N1/15E5/N2-2	CCCTCTGCTCGTCACGGCGT[T/A]ACGCAGTTCTCGGATCTGAC
85/15E5/86-1	CGAGGATCACTTCTCTCTGT[G/T]CAAGAAGAAGTTCGGCAAGG
85/15E5/86-2	GAAGAAGTTCGGCAAGGTCT[GA/AC]GCTTCCCGCGAGGAGCACGA
L1-15E9-86A	TCCACTCGCCGGGAAGAAAC[A/T]CGACAAACCGTTGTCTACTT
N1-15E9-86A	ATCTTCCTCTCTATCTTCAA[C/T]GTCGTGACAAGAATGATGTG
N1-15E9-86B	ATCTGCCTCTCTATCTTCAA[C/T]GTCGTGACAAGAATGATGTG
N1-15E9-86C	ATCTTCCTCTCTATCTTCAA[C/T]GTCGTGACAAGAATGAGTGG
N1-15E9-86D	ATCTGCCTCTCTATCTTCAA[C/T]GTCGTGACAAGAATGAGTGG
L1-15E9-86B	TCCACTCGCCGGGAAGAAAC[A/T]CGACAAACCGTTGTCCACTT
L1-15E9-86C	TCCACTCGCCGGGAAGAAAC[A/T]CGACAAACCGTTGTCTACGT
L1-15E9-86D	TCCACTCGCCGGGAAGAAAC[A/T]CGACAAACCGTTGTCCACGT
N2-15E9-85A	TCCACTCGCCGGGAAGAAAC[A/C]CGACAAACCGTTGTCTACTT
N2-15E9-85B	TCCACTCGCCGGGAAGAAAC[A/C]CGACAAACCGTTGTCTACAT
N2-15E9-L1	ATGGCTCGCGACGGGTCTCC[G/T]GTAAACCTCGGAGAGCAGAT
N2-15E9-86	GCCGACTCTCGAAGCTTCTT[A/]ACTCCACTCGCCGGGAAGAA

bl0702.oldlist

85/15E9/86-1	GAATCTAGGAGAGCAGATCT[T/G]CCTCTCTATCTTCAATGTTC
85/15E9/86-2	TCCACTCGCCGGGAAGAAAC[C/T]CGACAAACCGTTGTCTACAT
85/15E9/86-2B	TCCACTCGCCGGGAAGAAAC[C/T]CGACAAACCGTTGTCCACAT
85/15E9/86-2C	TCCACTCGCCGGGAAGAAAC[C/T]CGACAAACCGTTGTCCACGT
85/15E9/86-2D	TCCACTCGCCGGGAAGAAAC[C/T]CGACAAACCGTTGTCTACGT
85/15F1/86	GCAGGTAAAAATTCTACAGAC[C/A]TTCCCTTTTCATTGTAGTTA
85/15F5/86	TCTCCTCCGCCGCGCAAGAA[G/A]AAATCGACAGCGGCGCGTCT
85/15F10/86A	GTGCCCTAAAGATACCCTCA[A/G]GCTTGGTGTCTGCGCTAATG
85/15F10/86B	TTGCCCTAAAGATACCCTCA[A/G]GCTTGGTGTCTGCGCTAATG
N1-15E9-N2-1	GTCATGAAGATATTCACTAC[A/G]CCGACTCTCGAAGCTTCTTA
N1-15E9-N2-2	GCCGACTCTCGAAGCTTCTT[/A]ACTCCACTCGCCGGGAAGAA
N2-15G1-L3	TTCTTCCCACAGGTGAAACT[T/C]GCTAACTTCCTTCCAAAGTA
86-15H7-N2	CAGGACAATGTGTTTGTGAC[A/T]GTGGTTGCATCCATTCAATA
N1/15H7/N2	TATGTATCAGGACAATGTGT[GA/TT]GTGACTGTGGTTGCATCCAT
N1/15C10/N2	ACGGTGAGATCTAACGGCGG[G/C]GATCCTTCAGTCCATAGTCG
N1/16D6/N2	GCTAAGGTAGTTGGAGGAGC[CAA/GTG]CCACAGCCACGCGACTAAGG
N1/16A1/N2-1	GCTAAGCTACGCAACTGCCA[C/T]CAATCAGGGCAAGCTAAAGG
N1/16A1/N2-2	ATCAGGGCAAGCTAAAGGAA[C/T]GAATGACATTGAAGATGTGA
85/16A5/86	TATACACTCTTTAAAAGCGT[G/C]TGTGTGTACCCATCTCTCTT
85/16B6/N2A	GACATTTTCTAGACTTGAGA[T/]TGGCTGCGTATTGGCTGTCT
85/16B6/N2B	GGCATTTTCTAGACTTGAGA[T/]TGGCTGCGTATTGGCTGTCT
85/16B6/N2C	GGACATTTCTAGACTTGAGA[T/]TGGCTGCGTATTGGCTGTCT
85/16B6/N2D	GGGCATTTCTAGACTTGAGA[T/]TGGCTGCGTATTGGCTGTCT
85/16B6/N1	GGATCCATCTCAACTATGGT[A/C]GTATTATCGTTGAGGCTAGG
85/16B6/N1	TGGACCATCTCAACTATGGT[A/C]GTATTATCGTTGAGGCTAGG
N1/16B6/N2	ATGGCTGCGTATTGGCTGTC[C/T]AAGGCTGGATCTTGGTCCCA
85/16B7/86	GTATGTGATTCGGAAGAGAA[T/]CAAACTAAGTGCCGAGAAAG
86/16D6/N2	GCTAAGGTAGTTGGAGGAGC[CAA/GTG]CCACAGCCACGCGACTAAGG
85/16D10/86	CTCAACGTAGCAAGTAATAA[T/G]ATACTGTCTATTTATGGTTA
N1/16E9/N2A	AGACTTTCCCCATTCTCTTC[T/A]CCATCCACCGTCGAAACCCA
N1/16E9/N2B	TCACTTTCCCCATTCTCTTC[T/A]CCATCCACCGTCGAAACCCA
85/16H3/86-1A	ACTTCGAAACTGTAAACCTA[A/T]ACTTTAAGAGTTTAGAGCTA
85/16H3/86-1B	ATTTCGAAACTGTAAACCTA[A/T]ACTTTAAGAGTTTAGAGCTA

bl0702.oldlist

85/16H3/86-2a	CACCATCGGAGAAAGAGGTA[C/T]TTCGAAACTGTAAACCTAAA
85/16H3/86-2B	CACCATCGGAGAAAGAGGTA[C/T]TTCGAAACTGTAAACCTATA
85/17A5/86	CTAAGGCGTCTCCTGAAGAA[A/G]TACAGAGAGTCGAAGAAGAT
85/17C7/86A	CCGCGGACGACGCTTTCTTC[C/A]TCTGCTCCACCGCGAGCGCC
85/17C7/86B	GGGCGGACGACGCTTTCTTC[C/A]TCTGCTCCACCGCGAGCGCC
85/17F7/86	GAGGAGTAGTCTCCATGGCC[G/]AAGAAGAGCGTCGGAGACCTG
85/17G12/86	GAAGTTAGGGCTTCTAAGAT[C/T]AAGTTCGGCAAGGCTTTAAC
85/18A2/86	TCAAAACTAATATTTCTTTT[G/C]TTGATTGGTAATAAACAGGT
85/18A11/86	TTCCAGTGAAAAGGCATTGT[T/G]CTCCAAAATCTCGCTCTGCG
85/18A11/86	TCTGCTGAGACTGTGGCACC[/G]ATCTCGTTCTACGCCGGCTTC
85/18F5/86	AAGCAGCTCTGACTTGAATG[C/A]GAGAGGTTAATCAGACTGTG
85/18F5/86	AACTTGTTCTCTGATGGTGT[A/T]GTAAGTACGTGCGCCCCTTT
85/18H10/86-1	GTTTTTCTTTTGTTTGTTTT[A/C]TTAACTAGCGACTTGAAACT
85/18H10/86-2A	CATATTTTTCTCTCCCCTTA[G/A]ATTGAAGCAATCAAGAAGAT
85/18H10/86-2B	CATATTTTTCTCTCCCCTTA[G/A]ATTGAAGCAATCAAGAAAAT
85/18H10/86-3A	TAGATTGAAGCAATCAAGAA[G/A]ATCTCAGACTTCATCACCCA
85/18H10/86-3B	TAAATTGAAGCAATCAAGAA[G/A]ATCTCAGACTTCATCACCCA
85/19B3/86	GCATCCAACTCCAAGGATGA[/C]CCTGCCAAGGTGCTGCTAACT
85/19C8/86	GAGCTCAGGGATGGTGGATC[A/T]GACTACCTTGGAAAGGGTGT
N1/19F4/N2	TGGGGTTAGTCGAAATAGGT[A/T]AAATGCTTTGAGTATGTGTA
N1/19H1/N2	TACGCGCAGCACGGACTTGC[G/A]ACGCAAGCAATCGAGCTTTT
85/20B4/86-1	GAAGCCCATGGTACGGAGCG[G/A]GAGAGAGTCAAGTACTTGGG
85/20B4/86-2A	GAAAACGTCGCCAAGCCGAA[/G]GGGTCCATCAGGAAGCCCATG
85/20B4/86-2B	GTGAACGTCGCCAAGCCGAA[/G]GGGTCCATCAGGAAGCCCATG
N1/20B12/N2	AACGGGTCACTGCTAAATCA[T/A]AAGGATCACAAGGCTGGGAC
85/20C12/86	CTAGCCTACTTTGGGAAAAG[/T]TTCGTTATTGTTTTGTGTGG
85/20D2/86	GACTTCAAGGACTTCGCCGG[A/C]AAATGCTCCGACGCTGTCAA
N1/20D2/86	CGCGGGAGTGCTCACCTCCG[T/G]TCGACTCAGACCGTCGGCAA
85/20D3-D6/86-1A	AAGAGGCTGAGGGGGCTAAA[C/G]AGCAGGAAGAGCCTGAAGGA
85/20D3-D6/86-1B	GAGAGGCTGAGGGGGCTAAA[C/G]AGCAGGAAGAGCCTGAAGGA
85/20D3-D6/86-1C	AAGAGGCTGAGGGGGCTAAA[C/G]AGCAGGAAGAGCCTGAAGGA
85/20D3-D6/86-1D	GAGAGGCTGAGGGGGCTAAA[C/G]AGCAGGAAGAGCCTGAAGGA

bl0702.oldlist

85/20D3/86-2A	GAGGAGGGCTACATGCAGCT[G/A]AAGAGGCTGAGGGGGCTAAA
85/20D3/86-2B	AGGAGGGGCTACATGCAGCT[G/A]AAGAGGCTGAGGGGGCTAAA
85/20D6/86-1	GGAGGGGCTACATGCAGCTA[G/A]AGAGGCTGAGGGGGCTAAAG
85/20D6/86-2	AGGGGGCTAAAGAGCAGGAA[G/C]AGCCTGAAGGAGAGTTGGAA
85/20D6/86-3A	GAGTTGGAACTGAATGATGT[T/C]CAACCTATGAAGAAGAAACA
85/20D6/86-3B	GAGTTGGAACTGAATGATGT[T/C]CAACCTATGAACAAGAAACA
85/20D6/86-4A	GATGTTCAACCTATGAAGAA[G/C]AAACACCGAGGACCAACGAG
85/20D6/86-4B	GATGTCCAACCTATGAAGAA[G/C]AAACACCGAGGACCAACGAA
85/20D6/86-5	AGATGAAACACATCGCCAAA[/G]GATCCAAACACTCGAGAAAGA
85/20D6/86-5	CCATTAGTGAGGGAGCATGT[T/A]CCTGTCACATTTGATGATTG
85/20D6/86-7	AGCAGGAAGAGCCTGAAGGA[C/G]AGTTGGAACTGAATGATGTT
85/20D6/86-8	AAACACATCGCCAAAGATCC[CG/AA]ACACTCGAGAAAGAGTGGAG
85/20D6/86-9	ATCCTGTTGGTGAAGGATCA[C/G]TGAATCTGTCTTCTTACTTG
N1/20D8/N2	CTCATAGGCGATCTGGAGTA[T/G]GCAAATCGAATCTCCTCTCC
85/20C12/86	CTAGCCTACTTTGGGAAAAG[/T]TTCGTTATTGTTTTGTGTGG
N1/20E1/N2A	TGCACGCCTCACTTGTTCCT[T/A]CCAATCTGACATCAAGGATT
N1/20E1/N2B	TGCACGCCTCACTTGTTCCT[T/A]CCAATCTGACATCAAAGATT
N1/20F1/N2-1	NGTGTTTTTGAGGTGAAAGC[A/T]ACAAATGGAGATACCTTTTT
N1/20F1/N2-2	GANAAGACTTCGACAACACT[T/C]TGTTGGAGTNTTTGGTNTCT
N1/BoC-a2/N3-1	CCCATCTCATCCTTTCTTGA[A/G]CCGTTGAATCAAGCTCCTGG
N1/BoC-a2/N3-2	CCCGAGCCATTAGGACAAGA[T/C]GACTTGCCGTTTGACCAAAC
N1/BoC-a2/N3-3	TACATTCTCATTGGTTGGTT[C/A]TTGGGAAATAAAGTACCAAC
85-SC3-L2	GCACGCGCTAGAGTTGTTGC[C/A]AGAAGGAATGAACAATCTGA
86-SC3-L1	ATGGACGTTAAAAACGCTTT[T/C]CTTCCCGGAAATCTTGCTGA
86-SC3-N4-1A	TCCCGGAAATCTTGCTGAAA[A/C]CGTTTACCTGCGACAACCAG
86-SC3-N4-1B	TCACGGAAATCTTGCTGAAA[A/C]CGTTTACCTGCGACAACCAG
L1-SC3-N3-1	ATCTTGCTGAAACCGTTTAC[C/A]TGCGACAACCAGCCGGTTTT
L3-SC3-N5-1	AACAAGCCTGATCACGTTTG[C/G]TTGCTTCACAAATCTTTGTA
N1-SC3-N3-1	GAAGGCGTCCACTATCTTGA[A/G]ACCTATAGTCCTGTTGTTCG
N1-SC3-N3-1	GAAGGCGTCCACTATCTTGA[A/G]ACCTATAGTCCTGTAGTTCG
N3-SC3-N4-1	CTTGAGACCTATAGTCCTGT[A/T]GTTCGGTCCGCCACAGTTCG
N3/SC3/N5-1	CACAGTTCGTACAGTTCTTC[A/C]CATTGCCACTGTTATGCACT
L2/SC3/N3-1	AACCAGCCGGTTTTGTTGAC[C/A]GAAACAAGCCTGATCACGTT
L3/BL1/N5-1	ATGTCTTCAAAGTGCTCTGT[C/T]GCAACGCACGTCCGAACAAG
L6/BL1/N5-1	GTGCTCTGTTGCAACGCACG[C/T]CCGAACGAGAAAGACAACGA
2A7/2B7-1	GACGAGATGGAAAGCAACCA[T/G]AGGGTTCAGGAGAACCGGCT
2A7/2B7-2A	GAAAAATGCAAAATACTTAC[A/G]ACCTTGCTCAACAAGCTAAT
2A7/2B7-2B	GAAGAATGCAAAATACTTAC[A/G]ACCTTGCTCAACAAGCTAAT
2A7/2B7-3	CCTATAAAAGGGCCACGAGT[G/T]GAGATTGGGGGTCCTGGGGT
2A7/2B7-3	TGATGATGGATCTCAGGCTA[T/G]TCCGCATGGTAAAAACTACA

bl0702.oldlist

85 86	
2B7/2E7-1A	AGAGCACGCATTGGACCTAT[A/T]AAAGGGCCACGAGTTGAGAT
2B7/2E7-1B	AGAGCACGCATTGGACCTAT[A/T]AAAGGGCCACGAGTGGAGAT
2B7/2F7-1A	GCGGTTGCTGCTGGAGCTCA[A/G]AGAGCACGCATTGGACCTAT
2B7/2F7-1B	TCGGTTGCTGCTGGAGCTCA[A/G]AGAGCACGCATTGGACCTAT
2B7/2F7-2A	ATGCAGGGCAAGAGAGGGAC[G/T]CGGTTGCTGCTGGAGCTCAA
2B7/2F7-2A	ATGCAGGGCAAGAGAGGGAC[G/T]CGGTTGCTGCTGGAGCTCAG
S71G2/G6-1	ATAATACTTGATATGCCATT[G/T]TGTCCTCTTATTTTTAACAT
S67G1/G5-1	ATGGCCTCGTCGGCCACTGC[A/C]GTCGCTCCGTTCCATGGGCT
S67G1/G3-1	GCCGCTCCTCCAGAAGCCTC[G/A]GCAACGTCAGCAACGGCGGA
S67G1/G3-2	GTGTTGCCCATCCCATCCCA[A/T]TTCCCAACCCCAAACGAACC
S67G1/G3-3	GTACCTGCCGCCGCTGTCGA[CG/AC]GGACGACCTGCTGAAGCAGG
S66G2/G3-1	AGTGAGCCCGCTTCTTATTC[/T]TAAGGTGATAGGTTTCTAAA
S66G1/G3-1	AATGTAATGGTACTCCGCGC[T/C]ATGGCTCTGGTACTTAGGAA
S66G1/G2-1	AAATAGGCTCGGGCAATTAT[C/]CAGCTTAGGGACAGCAAGCG
S65G3/G6-1	TCCGCCCTGCCTCCGGTTTT[A/T]GCCCGACCTTCGAAACATTC
S65G3/G6-2	ACCACTGACGTAGCACCTCC[G/T]ACTTCTCGTTGTAAAACCCC
S65G3/G5-1	GGAGGTTCGCCTCATGTTAT[C/T]GTTGACGAGCCACATCCACT
S65G4/G6-1	GCTCCGACTTCCAATCTTGA[A/C]CCTCCACCCTGCCTCCGGTT
S64G1/g3-1	CTGGTTGAAATGTGTTGAAG[C/A]TACTAGTGATGAACTGCTTG
S64G1/g3-2A	GCTGCTCCAAGCGAGCCCGC[C/G]CCGAAAAAGGAAAAAGGTGA
S64G1/g3-2B	GCTGCTCCAAGCGAGCCCGC[C/G]CCGAAAAAGGAAAAAGTTGA
S64G1/g3-3A	CGCCCCGAAAAAGGAAAAAG[G/T]TGAAGGTCCTTACTCACCGA
S64G1/g3-3B	CGCGCCGAAAAAGGAAAAAG[G/T]TGAAGGTCCTTACTCACCGA
S64G1/g3-4A	GAACCGGCCACAGTGCCTGA[T/A]TTTGGCGGTGAGACCTCTTC
S64G1/g3-4A	GAACCGGCCACAGTGCCTGA[T/A]TTTGGCGGTGAGACTTCTTC
S63G5/G6-1	CAATTGTTACCTGAGCAAGA[T/]TTTTGTGTACTTGACTTGTT
S63G4/G6-1	TACTGAGAGAATGCAACATC[C/G]AGCATTCTGTGATTGGAGTC
S63G4/G5-1A	TTTTAGTGTACTTGACTTGT[C/T]CTCCTCCACAGATGAAATAT
S63G4/G5-1B	TTTTTGTGTACTTGACTTGT[C/T]CTCCTCCACAGATGAAATAT
S63G3/G6-1	TCTGTGATTGGAGTCTGCTC[G/A]CGTGTCAGCTCTGGATGTGA
S57G5/G6-1	AACTACAAAAAGCATCTCGT[G/T]GGATTTGGCTATCTCCTTTT
S57G2/G5-1	TTAGCGCGAAAAAAAAAACTC[/T]TTTTTTTTTGTCCTTTTACT
S57G2/G3-1	TCAATCCAATCAATTTAATT[T/C]CTTCCTTTAAAAATATTATC
S57G1/G2-1	TTACTACGAAAAACTCTTGA[G/T]TCTAGGAATTTGAATTTGTG
S57G1/G2-2A	CTTCTTGGATTTTGCTATCT[T/C]CTTTTACTACGAAAAACTCT
S57G1/G2-2B	CTCCTTGGATTTTGCTATCT[T/C]CTTTTACTACGAAAAACTCT
S57G1/G2-3A	TTTTACTACGAAAAGCATCT[T/C]CTTGGATTTTGCTATCTTCT
S57G1/G2-3B	TTTTACTACGAAAAGCATCT[T/C]CTTGGATTTTGCTATCTCCT
S57G1/G2-4	GAAGCCAAATCCTATTATTT[T/C]CTGCCTCTAGGGTCTGAATG
S56G4/G6-1	GTACACTGTTACAATCACAC[T/G]TAGTGAAGCGCAACACAGAT

Maize marker (start)

bl0702.oldlist

S56G4/G6-2	GCCTTATCATCCTCTAGGTA[T/A]TGGAGACGAGTGACCAGTCT
S56G4/G6-3	CTTTTCTTCAGACCCGAGCC[C/T]CCAATCGCGCCCTTCTGTGC
S56G4/G6-3	CTTTTCTTCAGACCCGAGCC[C/T]CCAATCGCGCCCTTTTGTGC
S56G4/G5-1A	GAGCCCCCAATCGCGCCCTT[C/T]TGTGCCTTGGCCTTGAGCTC
S56G4/G5-1A	GAGCCTCCAATCGCGCCCTT[C/T]TGTGCCTTGGCCTTGAGCTC
S55G1/G3-1	GAAGGAGCAGCAGCGCAAGG[A/]ACGTGTTCCAAGTCAACGTC
S54G2/G3-1	GTAGAAAGTTAGCAAAAACA[T/]TTTTTTAGTGAAAAAACATA
S54G2/G3-2	ATTGTGGCTAGAAACTTTGG[/T]TTTTTTTAAATTATGGTCAT
S53G5/G6-1	GCAAACCAACACCAATCTTC[G/C]AAATGAGCAAAGCAGAGACT
S53G5/G6-2	CAGATCGGTTGTCCTCAGAG[A/]AAGTCACCTACCTGCAAACC
S53G5/G6-3	AATTCTACATAGGAGTCATG[C/T]ACAAGTACTTGTTTAAAGGA
S53G5/G6-4	ACAAGTACTTGTTTAAAGGA[C/]CATGCCGGAATACACGCTGC
S53G5/G6-5A	GAGCGAGATCGATCCTGTTG[T/C]CATCCATCACTGCCATAGGA
S53G5/G6-5B	GAGCGAGATCGATCCTGTTG[T/C]CATCCATCACTGCCGTAGGA
S53G4/G6-1	TAGTCATAGCAACAGCATGC[G/A]TCGTGATGTAGCGTTCACCC
S53G4/G6-2	CAATTGAAGAGGAAAAAAAA[/T]TCTACATAGGAGTCATGTAC
S53G4/G5-1	CAGAGACTCCACAAGGCGAA[A/C]GGAGTCCACAATAGTTCGTC
S53G3/G5-1	CCCACGGCGGGAGATGGTGG[T/]TAGAAGCGGAACCACCGAGC
S53G2/G6-1	ACTTGTTTAAAGGACATGCC[G/]GGAATACACGCTGCCCAGGC
S53G2/G3-1	CCCAGGCCTTCCCACGGCGG[A/G]GATGGTGGTTAGAAGCGGAA
S53G1/G6-1	CAAAGCAGAGACTCCACAAG[A/G]CGAACAGAGTCCGCAATAGT
S53G1/G6-2	GAACAGAGTCCGCAATAGTT[T/C]ATCCTAATGCTACTTCGAGC
S49G2/G6-1	TGCTGCTGCACTTGCTCATC[G/C]TTACTGATTTGCTGAAATGT
S49G2/G4-3	TGCTGTAAAAAACGAGTGGA[C/G]TCCTAGTGTGTCGTGCGCTG
S49G2/G4-3B	CGCTGTAAAAAACGAGTGGA[C/G]TCCTAGTGTGTCGTGCGCTG
S49G1/G6-1	TGGCTCTAGCGAAGCGTAAA[GA/]GAGCAACGAAAGCAAGCGAG
S49G6/G1-3	TTTGCGCGCAATAAATCAGA[A/G]AGCTGATCTGAATCTGACCC
S49G5/G1-2	CAAGCAAGCAAGCTGTCTGT[C/T]CGTATGTGTCTGGCATGTTA
S49G1/G4-1	CGCTGTAAAAAACGAGTGGA[C/G]TCCTAGTGTGTCGTGCGCTG
S49G1/G4-2	TCTAGCGAAGCGTAAAGAGA[G/T]CAACGAAAGCAAGCGAGCGA
S49G1/G4-2B	TCTAGCGAAGCGTAAAGAGA[G/T]CAACGAAAGCAAGCGAGCAA
S49G4/G1-1	GTAAAGAGATCAACGAAAGC[A/G]AGCGAGCAAGCAAGCTGTCT
S49G1/G3-3	TGATTTGCTGAAATGTTGGC[G/T]TTTTTCTTGGTTGTTGGCCG
S49G1/G3-3B	TGATTTGCTGAAATGTTGGC[G/T]TTTTTCTTGGTTGTTGCCGG
S49G4/G6-2	CGCTGTAAAAAACGAGTGGA[G/C]TCCTAGTGTGTCGTGCGCTG
S49G4/G6-2B	TGCTGTAAAAAACGAGTGGA[G/C]TCCTAGTGTGTCGTGCGCTG
S49G4/G6-3	CTCTAGCGAAGCGTAAAGAG[AT/]CAACGAAAGCAAGCGAGCGA
S49G4/G6-3B	CTCTAGCGAAGCGTAAAGAG[AT/]CAACGAAAGCAAGCGAGCAA
S49G4/G5-1	CGGTGACCCGATGATTATGG[T/C]GGCGGCCACACCTGCAATGA
S49G4/G5-1B	CGGTGACCCGATGATTATGG[T/C]GGCGGCCACACCTCAAATGA
S49G4/G2-1	CGCTGTAAAAAACGAGTGGA[G/C]TCCTAGTGTGTCGTGCGCTG
S49G1/G6-1	TTTGCGCGCAATAAATCAGA[G/A]AGCTGATCTGAATCTGACCC
S49G1/G6-2	TGCTGCTGCACTTGCTCATC[G/C]TTACTGATTTGCTGAAATGT
S49G1/G6-3	TGGCTCTAGCGAAGCGTAAA[GA/]GAGCAACGAAAGCAAGCGAG
S49G1/G5-1	TGATTTGCTGAAATGTTGGC[G/]TTTTTCTTGGTTGTTGGCCG

bl0702.oldlist

S49G1/G4-1	TCTAGCGAAGCGTAAAGAGA[G/T]CAACGAAAGCAAGCGAGCGA
S49G1/G4-1	TCTAGCGAAGCGTAAAGAGA[G/T]CAACGAAAGCAAGCGAGCAA
S49G3/G6-1	CCACCCCGTTGCAGTGCTGT[/T]GCTGCTGCACTTGCTCATCG
S48G3/G6-1	GATTCAGAAACAGTGGCGGC[A/G]GATGTAGCATCAACACGCCC
S47G1/G3-1A	CACTCCTCCAAGATCTTATG[/A]AATCGTTCTGAGCTTATCGG
S47G1/G3-1B	CACTCCTCCAAGATCTTATG[/A]AATCGTTCTGAGCTTATCGC
S47G1/G3-2	GCAAGCTGGAGCACGGTACT[A/G]TAGTAGCGGCCGGCGAGGGA
S47G1/G3-3	GGAATACTCGATAGGCTCCC[A/G]CTGTGGGTAACAGTATTCCT
S47G1/G3-4	CTCCTCGTGGTAGTGACGAT[G/C]ATTGCATCGGTGCCACAGGC
S46G5/G6-1	CCCCCCACCAGCACCACCGG[/CC]CCCCGGCCAATTGGACCCAA
S46G3/G6-1A	GAAACAAGGGATAAAATGGG[G/A]AAAAAATCATTTTCCCTGAC
S46G3/G6-1B	GAAACAAGGGATAAAATGGG[G/A]AAAAAATCATTTTCCCTAAC
S46G3/G6-2A	GGGAAAAAAATCATTTTCCCT[G/A]ACCTTTACCACCACCATTAC
S46G3/G6-2B	GGAAAAAAAATCATTTTCCCT[G/A]ACCTTTACCACCACCATTAC
S46G3/G6-3	CAATTGGACCCAAACCAAAA[A/C]CAAACCCAACGGCTTTTCCT
S46G2/G6-1	CGCGGTTTTCCCGGCGGCTA[T/C]GCGGGCGGGCCGCCGGCCCA
S46G1/G6-1A	GCGGGCGGGCCGCCGGCCCA[A/T]CGTAACCTACCACCGTATTT
S46G1/G6-1B	GCGGGCGGGCCGCCGGCCCA[A/T]CGTAACCTACCACCGTACTT
S46G1/G2-1	TTCGGTGTCACTGACCTGTA[G/A]CATCAGCAGTAGCAGCGCCC
S45G5/G6-1	ATGAGTATATTCAAGTCATA[T/C]TGTGAACTAGAATGTTATTT
S45G5/G6-2A	CCTAGACGCTGACCGCCACA[G/A]ACGGCGGCGGCTGCCAAATC
S45G5/G6-2B	CCTAAACGCTGACCGCCACA[G/A]ACGGCGGCGGCTGCCAAATC
S45G5/G6-3	TGAACAAACCATGCGCTACC[C/T]AGCTAGGTGTTTTAAAGTAA
S45G4/G6-1	TCCGCGGAAACAACATCCGA[G/T]TTCTTGAGGATAACCCAGCT
S45G4/G5-1	GGGAGGGGAAAAAAAAAAGAA[G/A]AGCGTTGGTTGCGGTTCAGT
S45G4/G5-2	GGCGGCTGCCAAATCCGCGG[/A]AAACGACATCCGAGTTCTTG
S45G2/G4-1A	CTAGAATGTTATTTCTTCAC[C/A]GTTGACCATGGAAAAAAACA
S45G2/G4-1B	CTAGAATGTTATTTCTTCAC[C/A]GTTGACCATGGAAAGAAACA
S45G2/G4-2A	TTCACCGTTGACCATGGAAA[A/G]AAACAGTAATAAGTTCTTGT
S45G2/G4-2B	TTCACAGTTGACCATGGAAA[A/G]AAACAGTAATAAGTTCTTGT
S45G1/G6-1	TTCTTCACAGTTGACCATGG[/A]AAAAAAACAGTAATAAGTTC
S45G1/G5-1A	GAACCCACCGTGCCCTGGGA[/G]GGGAAAAAAAAAAGAAGAGCG
S45G1/G5-1B	GAACCCACCGTGCCCTGGGA[/G]GGGAAAAAAAAAAGAAAAGCG
S45G1/G5-2A	TGGGAGGGAAAAAAAAAAGAA[G/A]AGCGTTGGTTGCGGTTCAGT
S45G1/G5-3	CGTACCAGCTAGGAATCGTA[A/G]AAAAGCCTAGACGCTGACCG
S44G5/G6-1	GCTGCGTCAATCATCACTTC[T/A]CCCACAGGCGTCAAGTACAG
S44G3/G4-1	GACAGATTCCAAAGTAGTCG[C/T]CGGCCAGGTCGAAAAAGAAT
S44G2/G6-1	GGCGCTGCGTCAATCATCAC[A/T]TCACCCACAGGCGTCAAGTA
S44G2/G4-1A	TCGGTGTCACCACATGCATA[T/G]TCAGGACAGATTCCAAACTA
S44G2/G4-1B	TCGGTGTCACCACATGCATA[T/G]TCAGGACAGATTCCAAAGTA
S44G2/G4-2A	GTCGCCGGCCAGGTCGAAAA[G/A]GAATACTCAGCAAAAGACCC
S44G2/G4-2B	GTCGTCGGCCAGGTCGAAAA[G/A]GAATACTCAGCAAAAGACCC
S44G2/G3-1A	TATTCAGGACAGATTCCAAA[C/G]TAGTCGCCGGCCAGGTCGAA
S44G2/G3-1B	TAGTCAGGACAGATTCCAAA[C/G]TAGTCGCCGGCCAGGTCGAA

bl0702.oldlist

S44G1/G6-1	GCGTCAAGTACAGATACGCA[A/G]CACGCCTCAGCTTCGCCTTG
S44G1/G2-1	CCTGGGACTCCGCAAATTGC[G/A]AGCACTCGGTGTCACCACAT
S43G2/G6-1	GCTGGTTCATTATCTGACCT[G/T]GATTGCATTGCAGCTACAAG
S43G2/G6-2	CTGGATTGCATTGCAGCTAC[A/G]AGAAGCCCGTGGAAGGCCGG
S43G2/G6-1B	GCTGGTTCATTATCTGACCT[G/T]GATTGCATTGCAGCTACGAG
S43G2/G6-2B	CTTGATTGCATTGCAGCTAC[A/G]AGAAGCCCGTGGAAGGCCGG
S43G2/G6-3	TCAGCCCCTACTACGCCGAA[G/]GAGCTCATCTCCGGCATCGC
S43G2/G5-1	TACCCGGAGCTGAACCTCCC[C/G]GAGAGATTCAAGTCGTCCTT
S43G2/G4-1	TGCATGTGAACATTCATGAA[T/C]GGTAACCCACAACTGTTCGC
S43G6/G1-1	CTCCTACCAGGGCCGGTTCG[T/]CCTTCTCCGACTACCCGGAG
S43G1/G6-1	TGAATGGTAACCCACAACTG[C/T]TCGCGTCCTGCTGGTTCATT
S43G1/G5-1	GCCGACAGGGTCCTCACCGT[G/C]AGCCCCTACTACGCCGAAGA
S43G2/G6-1	GCTGGTTCATTATCTGACCT[G/T]GATTGCATTGCAGCTACAAG
S43G2/G6-1B	GCTGGTTCATTATCTGACCT[G/T]GATTGCATTGCAGCTACGAG
S43G2/G6-2	CTGGATTGCATTGCAGCTAC[A/G]AGAAGCCCGTGGAAGGCCGG
S43G2/G6-2B	CTTGATTGCATTGCAGCTAC[A/G]AGAAGCCCGTGGAAGGCCGG
S43G2/G6-5	TCAGCCCCTACTACGCCGAA[G/]GAGCTCATCTCCGGCATCGC
S43G2/G4-1	TGCATGTGAACATTCATGAA[T/C]GGTAACCCACAACTGTTCGC
S43G2/G3-1	CTGGTGGTGGTGCTTCTCTG[AAAC/]TGAAACTGAAACTGACTGCA
S43G2/G3-3	GACCATCTTCACGTACTACC[TACC/]AGACCGCTTTCTGCATCCAC
S43G1/G6-1	CTGACCATCTTCACGTACTA[CCTA/]CCAGACCGCTTTCTGCATCC
S43G6/G1-1	CTCCTACCAGGGCCGGTTCG[T/]CCTTCTCCGACTACCCGGAG
S43G6/G1-1	GAGATTCAAGTCGTCCTTCG[G/]ATTTCATCGACGGGTCTGTT
S43G1/G6-2	TGAATGGTAACCCACAACTG[C/T]TCGCGTCCTGCTGGTTCATT
S43G1/G6-3	GCCGACAGGGTCCTCACCGT[G/C]AGCCCCTACTACGCCGAAGA
S43G1/G5-1	TCTGACCATCTTCACGTACT[ACCT/]ACCAGACCGCTTTCTGCATC
S43G1/G4-1	CTTGATTGCATTGCAGCTAC[G/A]AGAAGCCCGTGGAAGGCCGG
S43G1/G4-1	CTGGATTGCATTGCAGCTAC[G/A]AGAAGCCCGTGGAAGGCCGG
S43G1/G3-1	GCTGGTTCATTATCTGACCT[T/G]GATTGCATTGCAGCTACGAG
S43G5/G6-1	AGAGATTCAAGTCGTCCTTC[G/]GATTTCATCGACGGGTCTGT
S42G6/G7-1	CTTTTAGGCCTTGACAAATC[A/G]CAATCCGGCCCCTTTTGATC
S42G6/G7-2	CTGCACTTGTGCAGACCATC[A/G]CCCTGATCGCTGTCAGGGAG
S42G5/G7-1	CTTTGCTCTGCACTTGTGCA[A/G]ACCATCGCCCTGATCGCTGT
S42G5/G7-2	TCGCTGTCAGGGAGGGCGTC[T/G]TGCAGCTCGGCTCCATGAAA
S42G5/G7-3	CAGCTCGGCTCCATGAAAAA[G/]GTGCCGCTACTCTCTCAGTC
S42G2/G7-1	GTTCTCTGCACTCCGATTGA[G/A]GGTCCGAAGCAGGGCAGCGC
S42G2/G6-1	CTCCATGAAAAAGGTGCCGC[/G]TACTCTCTCAGTCAGCTACT
S42G2/G3-1A	CTGCACTCCGATTGAGGGTC[C/G]GAAGCAGGGCAGCGCGTGTG
S42G2/G3-1B	CTGCACTCCGATTGAGGGTC[C/G]GAAGCAGGGCAGCGCGTTGT
S42G2/G3-1C	CTGCACTCCGATTGAGGGTC[C/G]GAAGCAGGGCAGCGCGTTTG
S42G2/G3-1D	CTGCACTCCGATTGAGGGTC[C/G]GAAGCAGGGCAGCGCGTTTT
S42G1/G7-1	CAGCTCGGCTCCATGAAAAA[G/]GTGCCGCTACTCTCTCAGTC
S41G2/G5-1	GATAGCCACATAGAACCTAT[G/T]CCTCCAGCTAACAACACGAG
S41G2/G5-2	CCCTCTTGACTCCTGCCGAT[T/G]GAGAAATAATTTTTTAGTAT
S41G5/G2-1	TTAGTATACCCATGACTATC[T/]TACTAAACTCTGTCAAAGCT
S41G2/G4-1	TGACTCCTGCCGATTGAGAA[A/G]TAATTTTTTAGTATACCCAT

bl0702.oldlist

S41G3/G1-1	CGCCAGATGAACCAGCTCAC[TA/AGT]ATCCTGCAAGAGATATCCCT
S41G1/G3-1	TTGCAATCAGAGAACATCGA[T/C]CAATAACTGACCTTGCTTTG
S40G5/G4-1	ACAATAAATGTATTAATATA[T/C]TTTTTATAAATTTAATTGAA
S40G4/G2-1	AAGTACATGACACCTCCGGA[G/A]ATACGGCCAAGAATCCCGCA
S40G4/G1-1	AGACGCTTGAAACGCATAAG[T/]TACATGACACCTCCGGAGAT
S40G1/G4-1	TTCCGTATGGACCAATCCAT[/C]CACGGCTTTGGAGCTTAACG
S40G1/G4-2	GGAGCTTAACGATACCAATC[GA/CG]AAATTCCCTCGCCGGGCAC
S38G5/G7-1	GAGATATATGGTACTTCTAG[G/T]AGATTCAAAGACATGGAGCA
S38G5/G7-2	ATAATGATGGAACCATGACT[G/A]CCGAAGATGAACCAACCTTG
S37G6/G2-1	GGTCAATAAGATAACTACAC[C/A]AAACTCTGCGTACAGTCTCG
S37G2/G6-1	GTCACTTACTCTGCTCGTGG[A/]AAGAAGTACTTGCCCTGCAG
S37G2/G5-1	GTCACTTACTCTGCTCGTGG[A/]AAGAAGTACTTGCCCTGCAG
S37G2/G4-1	TCTTATCAATTCTGTGCATT[C/T]AATACGATCAGCCAGACAGT
S37G2/G4-2	TCTTATCAATTCTGTGCATT[C/T]AATACGATCAGCCAGACAGC
S37G2/G4-3	AATTCAGCTCAAATCATAGG[T/G]CAATAAGATAACTACACAAA
S37G2/G4-4	GTCTCCCGGATCCAGAATCC[C/T]ACCGCGTTACATCGCCTTTC
S37G2/G3-1	CAGCGACAACATGCATAAAA[G/T]AGCAGGTCCAATTCAGCTCA
S37G3/G2-1	CCTTTCGGCCGCTCAGGGCA[/T]AACAAAATCCCCTCTACGCC
S37G3/G2-2	GCGTCACTTACTCTGCTCGT[/G]GAAAGAAGTACTTGCCCTGC
S37G2/G3-2	TGCAGGCGGCAGCCGAAGCG[/A]ATCGAAGGCCTGACCGGTCT
S37G2/G3-3	ACATCGCCTTTCCCAAACCC[G/C]CCATCTCCCCAGGCCGCGGC
S37G1/G6-1	GGGCAATAAGATAACTACAC[A/C]AAACTCTGCGTACAGTCTCG
S37G1/G6-1B	GGTCAATAAGATAACTACAC[A/C]AAACTCTGCGTACAGTCTCG
S37G1/G6-2	AATTCAGCTCAAATCATAGG[T/G]CAATAAGATAACTACACCAA
S37G1/G6-3	CAATACGATCAGCCAGACAG[C/T]CACTGTGCAACATCAGCAAA
S37G1/G6-3	CAATACGATCAGCCAGACAG[C/T]CACTGTGCAACATCAGCGAC
S37G1/G6-4	CTCCTTTCGGCCGCTCAGGG[C/A]AGACGAAATCCCCTCTACGC
S37G1/G6-5	CGAAATCCCCTCTACGCCCG[C/T]AGTGCTCCGCTAATCGATGG
S37G1/G5-1	AAGGGAGGGTGATCTCGGGG[T/]TGTGCCAGAGGGATGGCGTC
S37G1/G4-1	CAGCCACTGTGCAACATCAG[CA/AG]AAAACATGCATGAAAGAGCA
S37G4/G6-1	GTCTCCCGGATCCAGAATCC[T/C]ACCGCGTTACATCGCCTTTC
S37G4/G5-1	ATCGATGGACAAGGGAGGGT[A/G]ATCTCGGGGTGTGCCAGAGG
S37G4/G5-2	CCATCTCCCCAAGGCCGCGG[C/G]GGAAGGCGAAAACGAATGCG
S37G4/G5-2B	CCATCTCCCCAAGGCCGCGG[C/G]GGAAGGCGAAAACGATGCGA
S37G3/G4-1	CCTTTCGGCCGCTCAGGGCA[A/G]ACGAAATCCCCTCTACGCCC
S37G3/G4-2	ATCGATGGACAAGGGAGGGT[G/A]ATCTCGGGGTGTGCCAGAGG
S36G2/G5-1	TTGTCATGACCAACAGTGTC[G/A]GTGGGGTGGTCTCGTTGGAT
S36G2/G5-1B	TAGTCATGACCAACAGTGTC[G/A]GTGGGGTGGTCTCGTTGGAT
S36G2/G5-1C	TTGTCATGACCAACAGTGTC[G/A]GTGGGGTGGTCTCGTTGGGT
S36G2/G5-1D	TTGTCATGACCAACAGTGTC[G/A]GTGGGGTGGTCTCGTTGGGT
S36G1/G6-1	TGTCACTTTTTAGTGGTGTT[C/T]AGACTAAGGATGCTGACATT
S36G3/G6-1	TCACTTTTTAGTGGTGTTTA[C/G]ACTAAGGATGCTGACATTCT
S36G3/G6-2	TCCTTCGAGCATGACAAGAT[G/A]TCTTCTCTTCCTTGTGCAAC
S36G3/G6-2B	TCCTTCGAGCATGACAAGAT[G/A]TCTTCTCTTCCTTGTGTCAC

bl0702.oldlist

S35G3/G6-1	TCTGAGATACATTCATTTAA[C/A]ATGTCAGATAAAGAAAACTC
S35G3/G6-1B	TCTGAGATACATTCATTTAA[C/A]ATGTCAGATAAAGAAAAGTA
S35G3/G6-3	TCCTTATAATATCGTTGATA[C/]CCCTGTTTGTCAGTTTGTAG
S35G3/G6-4	CACCAGTAGTCTGGTGGTAC[T/]TTTTTTTTSSGCATGTGGG
S35G3/G6-5	TGCATGTGGGCAGGTACATA[A/T]ATTAAACATTCTAGGTATTT
S35G1/G4-1	CATTGAGGATTAATACTTTT[G/T]GACATGTTTGTTAATTTTTA
S35G3/G6-7	TGCCGCCTCAAAATGGTTTA[A/G]ATCTTTAAGCTGTCTTCCAC
S35G3/G6-7B	TGCCGCCTCAAAATGGTTTA[A/G]ATCTTTAAGCTGTCTTCCTC
S35G2/G6-1	CACCAGTAGTCTGGTGGTAC[/T]TTTTTTTTGCATGTGGGCAG
S35G2/G6-2	TGCATGTGGGCAGGTACATA[G/T]ATTAAACATTCTAGGTATTT
S35G2/G6-3	GGTTCGCACCATATCATGAT[C/T]GGAATGCCGCCTCAAAATGG
S35G2/G3-1	CCTACTTGTAGAACAATAGA[G/A]GTGTTCTCTACCTCTGAGAT
S35G2/G3-2	GCTCGAACTTCTAGTTGATT[A/G]CATGATTGCTATTACTGTTG
S35G4/G5-1	GGTTCGCACCATATCATGAT[C/T]GGAATGCCGCCTCAAAATGG
S34G3/G5-1	CATGCCTCTGTTGATATTTT[G/C]GTGCACCTTTTGCTTGCAAC
S34G3/G5-2	GATTTTGTAGGTTGATGCAT[C/T]GTTTGATCTTTCTTATCTCC
S34G3/G5-3	TGCTTGCAACTAAATTAATC[A/G]TGCTCTATTTGACTAAGAGT
S34G3/G4-1	ACATGTCCAGGACGCATGGT[C/]CCCAATATTGTTGTTGGAAG
S34G3/G4-2	TTGATCTTTCTTATCTCCTT[/C]CGAATTTGTTCTGTGTTATA
S34G3/G4-2B	TTGATCTTTCTTATCTCCTT[/C]CGAATTTGTTCTGTGTATAC
S34G2/G5-1	TGTAGGACTTGGAGAGCTTG[A/G]TAATTTACACATGCCTCTGT
S34G2/G5-2	CATGCCTCTGTTGATATTTT[G/C]GTGCACCTTTTGCTTGCAAC
S34G2/G5-3	GATTTTGTAGGTTGATGCAT[C/T]GTTTGATCTTTCTTATCTCC
S34G2/G3-1	GAGACATTTCCTACTCAATA[C/T]AATTATTTGATGAAATTATT
S33G5/G6-1A	AGTATCACAGACTAATCTGA[A/G]TATCTGGTTGCCACGAAAAC
S33G5/G6-1B	AGTATCACAGACTAATCTGA[A/G]TATCTGGTTGCCACAAAAAC
S33G5/G6-2	TCAAAGTGGTGCAATCGCAA[T/C]CCACTTGGGCTTGCCGTGGT
S33G5/G6-3	CCACTTGGGCTTGCCGTGGT[C/]CGTATCGTACGCAGGTAGCA
S33G5/G6-4	AGCATTTTTTGTTTTGTTTT[T/C]CCTTGGCAGACAACAGACAG
S33G5/G6-5A	CAGTCCCGAGAATCCCAAAT[C/]CAGAAAAAGGTTTTGTTTTT
S33G5/G6-5B	CAGTCCCGAGAATCCCAAAT[C/]CAGAAAAAGGTTTTGTTTTA
S33G4R/G6-1A	GGCAGACAACAGACAGATCA[AG/CA]CATGCTTGCATTTACTCCCA
S33G4R/G6-1B	GGCAGACAACAGACAGATCA[AG/CA]CATGCTTGCATTTACTCTCA
S33G3R/G6-1A	GTGATCACAGACTAATCTGA[A/G]TATCTGGTTGCCACGAAAAC
S33G3R/G6-1B	GTGATCACAGACTAATCTGA[A/G]TATCTGGTTGCCACAAAAAC
S33G3R/G6-2A	TCTGAATATCTGGTTGCCAC[G/A]AAAACCGGGACACAAGAGAG
S33G3R/G6-2B	TCTGAGTATCTGGTTGCCAC[G/A]AAAACCGGGACACAAGAGAG
S33G3/G6-3	TCAGTCAAACTCAGTCCCGA[A/G]AATCCCAAATCAGAAAAAGG
S33G3/G5-1A	GGTTGCCACGAAAACCGGGA[C/G]ACAAGAGAGAAACTCAGAGT
S33G3/G5-1B	GGTTGCCACGAAAACCGGGA[C/G]ACAAGAGAGAAACTCAAAGT
S33G2R/G3-1A	ACGCATGCTTGCATTTACTC[C/T]CAGTCAAACTCAGTCCCGAA
S33G2R/G3-1B	ACACATGCTTGCATTTACTC[C/T]CAGTCAAACTCAGTCCCGAA
S33G1R/G2-1	TATTATTCAATTTTGAATAA[/G]GAAGGAAATTTTAGCACCTC
S32G3/G5-1	ATTAATAAATGCATCCTCTG[C/G]TAAAAAAACCCATTTTGAAT
S32G3/G5-2	ATGAATTGAAGCTCTGAATA[C/T]AGAATCCACCATTCTTCCGA
S32G3/G5-3	GAATCCACCATTCTTCCGAA[A/G]CTGCTTCCTACAAAACTCGA

bl0702.oldlist

S32G3/G5-4	GAAAGGATGTGTTTTTGATA[G/A]CCTTCAGTCTTTCAGATGGA
S31G3/G5-1	CAATGTCTTGTTCGTTATCA[A/G]CGAAAGTTTGAATCCCCACA
S31G3/G4-1	TGTATCGGCTAGTCTGGATG[G/A]TCGCACTGGCACTCAGTGCT
S29G4/G5-1	TCTATTCAGCAGTCTGAGAA[GCA/CT]AGGATGGTCGGCTTCTTCAG
S29G1/G5-1	CCTTACACTATTAACAGGCC[C/T]GTGATCTACCTGAATGCCTG
S28G5/G6-1	CAAGAAGCCTCTTCAGTGTC[A/C]GTCGTAGCTTCCTCAAGACC
S28G5/G6-2	AGACCTTCCTGATGTGCGGA[T/C]GCTAATCCATGGAGCAGGGA
S28G5/G6-2B	AAGACCTCCTGATGTGCGGA[T/C]GCTAATCCATGGAGCAGGGA
S28G5/G6-3	CTAATCCATGGAGCAGGGAG[G/A]AAGGGGCGAGGGGCAGCAAG
S28G4/G5-1	TCGTCGCGAATACAGCCGGG[G/C]GAGGGGGTGGTCGCGACTGG
S28G3/G6-1	GTCGTAGCTTCCTCAAGACC[T/]TCCTGATGTGCGGACGCTAA
S28G3/G4-1	GAGTCGTCCCGAATACAGCC[A/G]GGGGAGGGGGTGGTCGCGAC
S28G3/G4-2	AGGGGGTGGTCGCGACTGGA[T/G]CGCCCGAGCAGCGAGCAAGC
S28G3/G4-3	AAGCACATGTTTTAACCTTT[T/G]ATTCAAACTTTCCAGCCGTT
S28G3/G4-3B	AAGCACATGTTTTAACCTTT[T/G]ATTCAAACTTTCCAGCGTTA
S28G2/G6-1	GAATGTTGCTGTTATATTAC[T/C]CGTAGGTGACAAAGGGTTCA
S28G2/G4-1	AGAAAAATTTACATAAAAAA[G/C]CACACTCCATGATTGTTAAA
S28G2/G4-1B	AGAAAAATTTACATAAAAAA[G/C]CACACTCCATGATTGTTTAA
S28G2/G3-1	CTTTTATTCAAACTTTCCAG[/C]CGTTAATTTGTTATCCGTTG
S28G6/G1-1	TGTTGAACATGCTCTCAGGA[/CC]CCCCCTATTGTGACACAGCA
S28G1/G3-1	TACATCTTAACAAGCACATG[TG/TTT]TAACCTTTTATTCAAACTTT
S27G3/G6-1A	AGTAATGTGTGACTGTGGGC[C/G]CGTGTGACAGCTTTTACGTA
S27G3/G6-1B	AGTAGTGTGTGACTGTGGGC[C/G]CGTGTGACAGCTTTTACGTA
S27G3/G6-2	TTCGCTTGGTAGCCGTAGCA[G/A]TATACTTTTACCGGCCACAG
S27G3/G6-3	GGGCTTTGGGTTGTGAACTT[CCA/C]AAAAAAAAAAAAAATTTCCC
S26G5/G6-1	CCAAGAAAGATTAATGCTGG[/T]TAAAATATTGTTTCCAGTCT
S26G5/G6-2	AAAATCAGGACTGCGAAAAA[A/C]CCAAGAAAGATTAATGCTGG
S26G5/G6-2B	AAAATCAGGACTGCGAAAAA[A/C]CCAAGAAGATTAATGCTGGT
S26G5/G6-3	AAAGTGTGTGTTGTTGCCCA[G/A]ATGATTCCATTCCACACAAG
S26G4/G5-1	AGGACTGCGAAAAAACCAAG[/A]AAGATTAATGCTGGTAAAAT
S26G4/G5-2	ATGCTGGTAAAATATTGTTT[/C]CAGTCTTTCACAAAGTGTGT
S26G3/G4-1	CTACAAAAATCAGGACTGCG[/A]AAAAACCAAGAAGATTAATG
S26G3/G4-2	TTGTTTCAGTCTTTCACAAA[/GT]GTGTGTGTGCCAGATGATTC
S26G3/G4-3	TCACACACCGACCTGCCTGG[/T]TATCAGGAACCATCCTCCTG
S23G4/G5-1	GGTGAATTGGTGATGCATGC[T/G]GGGGGTGCTCGAGTTGGATG
S23G4/G5-2	TTCCAGTCGGATGAACTGGA[T/G]GTTCGTCATCCACTCGTCAC
S23G3/G6-1	GGTGAATTGGTGATGCATGC[A/T]GGGGGTGCTCGAGTTGGATG
S23G5/G3-1	TTAAGTGAAGATGCCCAAAC[C/G]GTTAAACTTTCCATGGAACT
S23G5/G3-1B	ATTAATGAAGATGCCCAAAC[C/G]GTTAAACTTTCCATGGAACT
S23G1/G6-1	TGATTCGGGTCTGTATGCGA[G/T]TGTTGTGGTGGTGAACTGGT
S23G1/G5-1	CGGGTCTGTATGCGAGTGTT[G/A]TGGTGGTGAACTGGTGAATT
S23G1/G4-1	GTTCGCGGTTTCTGGGGCCG[G/T]GGGCGGTGCTCGGTGGGGCC

b10702.oldlist

S22G5/G6-1	CAGATTGGTGTCGTTTACTA[A/G]AATTCAGTTCTGTCCATTTG
S22G5/G6-2	AAGTAAGCATTCTTTATATG[/T]TACTTCCCATGATAAACTTT
S22G5/G6-3	CAAAGGGCTTACTGTACTTT[/C]CATCTTATTGGCAGGGCACC
S21G3/G7-1	AGGCACTGACGGTGCGATGG[/T]TTTGACCTTAATTGGCATTC
S21G3/G6-1	GTTCTCGCTGCCGTCACAAG[A/]ATTCTAGTAAGGTGTGGCTT
S21G3/G6-2	ACTGATCTCAATTATGCATG[/A]AGAATGTTTCTCGCATCAAG
S21G2/G7-1	TTGACGGTGTTAGTTTCGAG[A/G]AGATAACACACGCTGGGAAT
S21G2/G7-2	CGATTATTAGCACGCTGGGA[G/T]TTGACCTTGAGCTCCAGGGA
S21G2/G5-1	TGGCTTGGTTGACCTTGAGG[C/G]CCACACACTATCTAGTACGT
S21G2/G5-2	TCCAAGTCATCTGCTAACTG[A/]ATCTCAATTATGCATGAGAA
S21G2/G5-2B	TCCAAGTCATCTGCTAACTG[A/]ATCTCAATTATGCATGAAGA
S21G2/G3-1	AGTTTGACGGTGTTAGTTTC[G/A]AGAAGATAACACACGCTGGG
S21G2/G3-2	AGAATGTTTCTCGCATCAAG[T/]TGCTAGAGCTGGAAAACGAA
S20G5/G6-1	GCCGCCGAGAGCGAGGCATA[G/T]GCGCATGTGCATGTGCGTGC
S19G5/G6-1	ACTTGGCCGGGGACGTCGAC[G/A]ATCGTCGTAGCACTACTGGT
S19G5/G6-2	AGTACATGGCGAGCGTTGTA[G/C]CAGCTGCTTAGGTGATGTGG
S17G5/G7-1A	GCTCATCACTTTCTTTCCAC[C/T]GTTTTTTTAGATGTGCACCG
S17G5/G7-1B	GCTCATCACTTTCTTTCCAC[C/T]GTTTTTTTAGATGTGCACCT
S17G4/G7-1A	CTGTTAATACTTCTATTTCC[A/C]AGCTAACAACCCCTCTTGGT
S17G4/G7-1B	TGTTTAATACTTCTATTTCC[A/C]AGCTAACAACCCCTCTTGGT
S17G4/G7-2	CCTCTTGGTCCCAACATCCT[G/T]GAAAACTTCGGAAAAGGCTT
S17G4/G6-1	CTATTTCCAAGCTAACAACC[C/G]CTCTTGGTCCCAACATCCTG
S17G3/G7-1	TGGGCCTAACCAGTGATTTT[A/T]GGCTGAATCTTGTCTTGTGC
S17G3/G7-2	TCCTCTTGTGCTGTTACTGT[C/T]TTCTCTACTGCCTGTACTGA
S17G3/G7-2	TGCACCTATGTGTCTTATTA[A/T]CATGCGATTCTACTAGTTTA
S17G3/G7-3	AAGCCTCATGTGCAGATTCA[TC/AG]GAACACACAACGTCAGCCAT
S17G3/G7-4	ACAACGTCAGCCATGAGCCC[C/A]TGACACAAAGAATCTGCACT
S17G3/G6-1	GGTTCTAAACATAGCTCGTC[C/A]ATTCATGATTCATCTCGAGC
S16G6/G7-1	GTGCTTTCGTAAACCTAGAG[CT/TG]GACCAGCTGTGATTTCGATG
S16G4/G6-1	TCAGCAAGCCTCCAAGGCTC[C/A]AATGGTCCAGTTACTTGGTT
S16G2/G7-1A	TGCTTTCGTAAACCTAGAGT[T/G]GACCAGCTGTGATTTCGGTG
S16G2/G7-1B	TGCTTTCGTAAACCTAGAGT[T/G]GACCAGCTGTGATTTCGATG
S16G2/G7-2A	GTTGACCAGCTGTGATTTCG[G/A]TGTATTCCACGACCACGAGT
S16G2/G7-2B	GTGGACCAGCTGTGATTTCG[G/A]TGTATTCCACGACCACGAGT
S16G2/G6-1	GTGTGTAGCTTCATTCGCAA[TG/AT]TTTGAACAGCCTCTGCAAGT
S16G2/G6-2A	GTGCTTTCGTAAACCTAGAG[T/C]TGACCAGCTGTGATTTCGGT
S16G2/G6-2B	GTGCTTTCGTAAACCTAGAG[T/C]TGACCAGCTGTGATTTCGAT
S16G2/G6-3A	GCTGACCAGCTGTGATTTCG[G/A]TGTATTCCACGACCACGAGT
S16G1/G7-1A	CTTAATTGTACACAGTGCTT[C/T]CGTAAACCTAGAGTTGACCA
S16G1/G7-1B	CTTAATTGTACACAGTGCTT[C/T]CGTAAACCTAGAGTGGACCA
S16G2/G7-2B	TGCTTCCGTAAACCTAGAGT[T/G]GACCAGCTGTGATTTCGATG
S16G1/G6-1	TGTGTAGCTTCATTCGCAAA[G/T]TTTGAACAGCCTCTGCAAGT
S16G1/G3-2A	GTGCTTCCGTAAACCTAGAG[T/C]TGACCAGCTGTGATTTCGAT
S16G1/G3-2B	GTGCTTCCGTAAACCTAGAG[T/C]TGACCAGCTGTGATTTCGGT

bl0702.oldlist

S16G1/G2-1	GTGTGTAGCTTCATTCGCAA[A/T]GTTTGAACAGCCTCTGCAAG
S14G5/G7-1	CTGGACCAGATCGCCCTGCC[/TC]TCAGATTCAGAGATTGACGA
S14G5/G7-2	CGAAAGAGCGAGATATATCG[A/G]TCGATCGATGAGCAAGTATA
S14G5/G6-1	GCTCAGCTGCCGGAGTACGT[A/T]GGCTTGCTCTCCGGCCGGCC
S14G5/G6-1B	ATAGCTCTGCCGGAGTACGT[A/T]GGCTTGCTCTCCGGCCGGCC
S13G5/G6-1	TTTCACAACTCAACTGATTG[A/T]CTTGCTTTGATGTGGATTCT
S13G2/G6-1	TTGGTAATTTCAGAGCTAGA[C/G]AACTTACTGTGGTACACGCC
S12G4/G6-1	ACCTTTGCTGTGTTTTTTTT[T/G]GTATTCGAATGGAGGGAGTA
S12G2/G5-1	AAAACAGCCAAGGTGGTGGT[C/G]AAAGGAAGGTGTCAGAAGGT
S12G2/G5-2	TCTGTTCGTTCCATCTCTTT[A/G]CAGTAAATATCCGTAATTAC
S12G2/G5-3	CGTAATTACTTTGTTACTAC[TA/C]AGTAATTTTATATATATCCT
S12G2/G5-4	TATATATATCCTCATTTCAA[A/T]GAACAGTCAAAGTTAGTTTT
S12G2/G5-4B	TATATATATCCTCATTTCAA[A/T]GAACAGTCAAAGTAGTTTTG
S12G2/G4-1	TATTTCTTATCCAGGATTGT[T/C]CTTTGGCCAAAGCATGGTAC
S12G2/G4-2	CGTTCCATCTCTTTACAGTA[A/G]ATATCCGTAATTACTTTGTT
S12G2/G4-3	ATCCGTAATTACTTTGTTAC[TA/AC]CTAAGTAATTTTATATATAT
S12G2/G3-4	GTAATTACTTTGTTACTACT[A/]AGTAATTTTATATATATCCT
S12G1/G6-1	CTGTGTTTTTTTTTGGTATT[G/C]GAATGGAGGGAGTATTATTT
S12G1/G6-1B	GCTGTGTTTTTTTTGGTATT[G/C]GAATGGAGGGAGTATTATTT
S12G1/G5-1	ACTTAGATGATGACCAGGTG[A/]AGAGTTTGGCACCTTTGCTG
S12G1/G5-2	AGTTTGGCACCTTTGCTGTG[T/]TTTTTTTTGGTATTGGAATG
S12G1/G5-3	CTTTACTGATTGGGTTACAA[A/G]AGGTTATTTCTTATTCAGGC
S12G1/G5-4	AATTACTTTGTTACTACCAG[T/]TAATTTTATATATATCCTCC
S10G4/G6-1	AGCGACAGGGATGTCGAGCA[G/T]CTACGGAAGGCAATAATGAG
S10G4/G6-2	AATTTGGGAAAATCAATGCA[GAA/CAC]ATCAGTGATTAATCCACATA
S10G3/G6-1	GCATGGCGGAGTGAGGGAGG[TG/]TGTGTGTGTGGCTCCACA
S10G3/G6-2A	GGCCGCTACGCCATTTAGCG[G/A]ATTTGGGAAAATCAATGCAG
S10G3/G6-2B	GGCCGCTACGCCATTTAGCG[G/A]ATTTGGGAAAATCAATGCAC
S10G1/G6-1	CATCCCCGCCGGCAGAACAA[C/G]GTACGAGAAGGATGGAATGC
S08G5/G6-1	GTCCCAGATCAGGTCCACGT[T/C]CGAGCTCGCTGTTCCCGCTT
S08G5/G6-2	TGGTTCTTCACCACCACCGC[C/G]CCGGGCGCGCCCAGCGCCTC
S08G4/G6-1	GCAGCCTCAGGTACACGGGG[/A]AAGTCGGAGTGGTTCTTCAC
S08G4/G6-2	GCCGGGCGCGCCCAGCGCCT[/C]CGTCCCAGATCAGGTCCACG
S08G3/G6-1	GCACGTCGTTGGTGAAGAAG[AC/CA]GCGGTACGGGTGCTTGTCGA
S08G3/G5-1	AGGTACACGGGGAAGTCGGA[G/T]TGGTTCTTCACCACCACCGC
S08G3/G5-2	CGACGGCGTCCAGCACCGAC[G/]CCTCCGCCTTCACCCCGCGC
S08G3/G4-1	GTCCACGTCGAGCTCGCTGT[C/T]CCCGCTGCCCACGACGGCGT
S08G1/G4-1	GCACGTCGTTGGTGAAGAAG[A/C]AGCGGTACGGGTGCTTGTCG
S06G2/G3-1	NAACCAAACCCTGACTATTA[T/C]AGGTAGATTAGACTAGACAC
S06G2/G3-2	ACGGTGAGGAGTGGCACATG[A/C]GATGGAAAGTTCCTGTAGAC
S06G2/G3-2B	ACGGTAAGGAGTGGCACATG[A/C]GATGGAAAGTTCCTGTAGAC
S05G2/G4-1	TATGCTTGGAAAGTGGGAAA[G/]CGGAACATACGATGGAGGAC

bl0702.oldlist

S03G5/G6-1	AAACAATAATTTTTACACAG[/T]TGCTAAGGTTTTACTGTTTT
S03G2/G6-1	ATATCCATGTTGTCGCCTGC[/TG]TGTGCGCTTGCTTGCCGCTA
S02G6/G7-1	CACGGCAGTTGGCAGTGTGG[A/]AAGGACTATCTCGTGGTGAT
S02G6/G7-1	GTGGTGATGCCAACATGCAA[G/]TTACCCAATCCAGGCTTCCC
S02G4/G7-1	TGGTGTTTGTTAGGAAAGAC[T/C]TAATTTCACGGCAGTTGGCA
S02G4/G7-2	AATAATATTTGGCGGTGAAA[G/]CCTGGTGGAAAACTGTTTTC
S02G4/G7-2B	AATAATATTTGGCGGTGAAA[G/]CCTGGTGGAAAACTGTTTCC
S02G4/G6-1	TTGCTGCTATGTTTACTGGG[/T]TGTAGAAAAAAAAATAATAT
S02G3/G7-1	CAACGTGCAATAATAGAACA[T/G]GTGGTGTTTGTTAGGAAAGA
S02G2/G6-1	GCTCGGTAATAATTCTGGCT[C/G]CGATGGCACCCATATTCCTC
S02G2/G6-1B	GCTCGGTAATAATTCTGGCT[C/G]CGATGGCACCCATATTCCTG
S02G2/G5-1	AAAACACGTGGTGTTTGTTA[G/A]GAAAGACCTAGTTTCTCGGC
S02G2/G5-1B	AAATCACGTGGTGTTTGTTA[G/A]GAAAGACCTAGTTTCTCGGC
S02G2/G5-1	TAGTTTCTCGGCAATTGGCA[G/T]TGTGGAATGACCATCTCGTG
S02G2/G5-1B	TAGTTTCTCGGCAATTGGCA[G/T]TGTGGAATGACCATCTCGTC
S02G2/G5-2	GTGTGGAATGACCATCTCGT[G/C]GTGATGCCAGCATGCTGTTA
S02G2/G5-2B	GTGTGGAATGACCATCTCGT[G/C]GTGATGCCAGCATGCTACTA
S02G2/G5-3	ACCCTGTCAGGCTTCCACAG[A/C]TATAATATTTGTTGTGGTGT
S02G2/G5-3B	ACTCTGTCAGGCTTCCACAG[A/C]TATAATATTTGTTGTGGTGT
S02G2/G5-3C	ACTCTGTCAGGCTTCCACAG[A/C]TATAATATTTGTTGTGTGTG
S02G2/G5-3D	ACCCTGTCAGGCTTCCACAG[A/C]TATAATATTTGTTGTGTGTG
S01G7/G4-1	GAAAAGACGAGAGAGATTCC[G/A]AAAGCCCCATCTCCCCGACT
S01G7/G4-1B	GGAAAGACGAGAGAGATTCC[G/A]AAAGCCCCATCTCCCCGACT
S01G4/G7-2	AACAGCGCAAGAGTCAACAC[A/G]CGCGCGCATCACGCATGCCA
S01G4/G7-2B	AACAGCGCAAGAGTCAACAC[A/G]CGCGCGCATCACGCATACCA
S01G4/G7-3	GCTAGAGCAAGAGTCAACAC[G/A]CGCGCGCATCACGCATGCCA
S01G4/G7-3B	GCTAGAGCAAGAGTCAACAC[G/A]CGCGCGCATCACGCATACCA
S01G4/G7-4	CACACGCGCGCATCACGCAT[G/A]CCACGAGCTTTCAGGTTATG
S01G4/G7-4B	CACACGCGCGCATCACGCAT[A/G]CCACGAGCTAGCTTTCAGGT
S01G3/G7-1	CAGGCCGGCCCCGCCATTGG[/A]AAAGACGAGAGAGATTCCGA
S01G3/G7-2	AGCCAGGTTCTAACAGCTAG[C/A]GCAAGAGTCAACACGCGCGC

TABLE 3: PRIMERS PAIRS FOR AMPLIFICATION OF FRAGMENTS CONTAINING POLYMORPHISMS

NUM	FORWARD_PRIMER	REVERSE_PRIMER
1	TCTCGGATGCTAAAAAGCAAGC	TCGTGGGTTGATCTCGAGGAC
2	TCTGACATCTCTCAACGTCCTT	GAAAGTCTTCAGGGATCTTCCG
3	GGTGAGATCTTAAACACCTTAAAC	CGTTTTTAACTTTTGGTTAGATTG
4	CCCAATCCCCAAATTTAAAGCA	AGGGTACCAAAGGGTACATCAT
5	ATAGCAACTACTGATAGTGAACCA	ACTCTCTTTGCTTTAAATTTGGG
6	TCTCCCAACGTATTCTCTTGGT	TCTGCTCCCCTGCAACATTAAC
7	TCAGAGGCAAAGCGGTAGTTG	GTTGGGAGATTACCTCGTGAGA
8	TCCACTACCAGCTTCAATGTCT	CGTAATGAACTTTGGCATCGAC
9	CGATGCCAAAGTTCATTACGAT	TCGTGGTCTCCATGGATGACT
10	TCTCCTTACTTCCTTTCTTCCC	ATGAGTTTCTGCACTTTTCACT
11	TGACAATTTTGTTTTGTTTCTTG	TACAGAACTTTGTTCTGACCTGA
12	TGCTTTAAAAACCAGAGCCACC	TTTGGAAAGAAAGGAAACGATG
13	GGCAAACAATCTAAGCGGTC	CGAGCAAGAAGCATGAGACA
14	CCATGGTAGGACAGGCAAAC	AGTGAGACTGCGGTCGAAA
15	TCTAAGCAGTGCAACAGCTCCT	AGAGCTTCCTCGTACGTCAGGG
16	CAACAAACTCAAAAAAACGATACCT	AGCGAGACGGCGAGAGACG
17	TGTTGATCAGGAGACAGTTACA	TGAAGTTCGAGATCCTTGCGAC
18	GCTGCTCCTGATCTTGAAGG	TGCGACTCTGTGGGACTGTA
19		
20	GATAAGGTCCATGATGATGACA	GATCAGGTCCATGATGATGACA
21	CCATTGGTATACATCCAACTTT	TGATGACAAAAAAGGTATTCCA
22	AGGTCCATGATGATGACAAAAA	AAAGAACTGGAGAAAAGTTGGA
23		
24		
25	AAGGACACTCCACTTTCTTCGT	AAAGACATGAGACCGGCTCG
25	AAGGACACGCCACCGTCTTC	AAAGACATGAGACCGGCTCG
25	GACACTCCACTTTCTTCGTGGC	AGATGAAAGACATGAGACCGGC
26	TCTGCTGCAAGAGATGGTGTGT	TGTGAGTATCCATCGAAGAGGT
26	CATCGCTGTTATCATCAGTACC	AGAGGTAGTAAGAATTAGCCTTGG
27	TCTGCTGCAAGAGATGGTGTGT	TGTGAGTATCCATCGAAGAGGT
27	GCTGGTGTGTTGGGTATCTACG	ATTAGCCTTGGGGTTAATACCG
28		
29	GTTCTTGGTCTTCCTTACGCCT	GGAGGACACCCATGAGCCAG
30	CTGGACTATGCGGTGGCT	GATAGGAGCGAACGTGAAGG
31	GACTAGTGCGGTGGCTGC	GATAGGAGCGAACGTGAAGG
32	GACTAGTGCGGTGGCTGC	GATAGGAGCGAACGTGAAGG
33	AAACGGTACTGCGAAAGCTG	GGCACCACATCGAAGTTTCT
34	CCTGAAACGGTACTGCGAAAG	AAGTTTCTCAAGTTGTGGAATTC
35	CAACAACAAGCTGGTCAGGA	GCTTGAACGGAGCAGCAT
36	GTTTCTCGTCAAAAGCCACG	TCCAAGGCGCAAGAAGAG
37	ACAACCTCGCGGTGGTAAC	TCCAAGGCGCAAGAAGAG
38	AAACCAGGGTCCTTGATGTG	AGCTTGTTGTTGGAAGCGTT
38	TAAGACCAGTAAGCGGAAAACC	CTTGTTGTTGGAAGCGTTGTAG
39		
40	CTTTGGGACCGTTGGAGTT	TTTCCACCGTCATAGCCG
41	GATGGTTGTGGTAGCGACTGC	TTAAGGCTGCTTCCAGGCTC
41	GATGGTTGTGGTAGCGACTGC	TTAAGGCTGCTTCCAGGCTC
42	CTGATATGGAGGTTGAAGGAGG	CTTATTTGTCTCCGGTAGCTCG
43	TACGGTCCCATCAGTGACAA	GGCTCATTCCAGCCATTTC
44	GCTGCTCTAGGGATGCTCAG	TGTCACTGATGGGACCGTAA
45	CTAGGGATGCTCAGCACCATC	TGGGACCGTAAGCATCAATC
46	ATATGATGAGAAAGTGCTTGTGG	ATGTTGCGGTGCACGAGATT
47	ATATGATGAGAAAGTGCTTGTGG	ATGTTGCGGTGCACGAGATT
47	ATATGATGAGAAAGTGCTTGTGG	TTGTAGCGGTGCACGAGATT
48	ATATGATGAGAAAGTGCTTGTGG	TTGTAGCGGTGCACGAGATT
49	TGGGAATGATTGGTTTGAGA	CGATATATCAAGCGTACCAGC
50		
51	GGAGAAACCCTCTCCGACTT	GCCGAAGGTCATGGAGAAAG

52		
53	GTTATCGATCGCGTGGTCC	GGTGTCGGACAGGGATACTG
54	GTTATCGATCGCGTGGTCC	GGTGTCGGACAGGGATACTG
55		
56		
57		
58	AAAAACGAAACTGTTGCCTCA	GGCTACACCTTCATACCATGAAATA
59	TGGGTCTTGATGGATTGTTTC	CAGCTACCTCCATCAGCTTCT
60	TACCGTGCGAGAACAGAAGAGA	TCCTTAAGTACTGTCCGACGTG
61	AAACGTGTGACACAACGAAG	ACGGAACCCACGGCATTTAC
61	AAACGTGTGCCACAACGAAG	ACGGAACCCACGGCATTTAC
62	GATATCCAATACGGGTCCTAGC	AAATGCACCAGAAACGGTGAG
62	GATATCCAATACGGGTCCTAGC	AAATGCACCAGAAACGGTGAG
63	CTTGGGCTTTCGGTGGTAT	TGCAATAGACGAGGACGAAG
64	ATTAAAGCACAAAGGTCTGCCT	CGTTCCAGACACGACCAGTAC
65	CCATTTTAACCTCCTTGATTCC	ATAGTTAGAAAGACCCCCAGCC
65	CCATTTTAACCTCCTTGATTCC	ATAGTTAGAAAGACCCCCAGCC
66	GATCGAAGACGAGAGCTTGAA	GTATGAAGGTTTTCCAAATCCG
66	ACTAAAACGAGAGCTTGAATAACG	TGAAGGTTTTCCAAATCACCGT
67	GGAGCAAAGCTAAAAAGATCGA	CTCCAAGCTTGATAGATGGAGC
68	GTCCAATGGAAGGTGGGTTTAG	CCCACAGTGAAGTTTGTATCCA
69	TGGAAGGTGGGTTTACCGT	CCAAAGATGGTTCCCACAGT
70	ATTGGGTCTTGATGGATTGTTT	GACAGCTACCTCCATCAGCTTC
71	TGGATTGTTTCTATCCTGCAAA	AGCTACCTCCATCAGCTTCTA
72	TCTACCACGGTCGTACTGGTC	GCTTGGTGACGTTCCAGAC
73	TGGTTCTGTCTCATTTTGTTGG	CCATCAATATCTACGCTTTCGA
74	TGGTTCTGTCTCATTTTGTTGG	CCATCAATATCTACGCTTTCGA
75	GCCAAAACACTGTTGGAGGAC	GTGTCCCAGATGTTGTCTTGAA
75	CCGAAAACACTGTTGGAGGAC	GTGTCCCAGATGTTGTCTTGAA
76	ATTACCCCCGTCTTTCGTATCT	TAAGGTATTTGCATCTGATCGG
77	AATGAGATCATAGTATCCGCCG	TAGTTGAGATGATGGCCCGAC
77	AATGAGATCATAGTATCCGCCG	TGTAGTTGAGCTGATGGCCC
78	AATGAGATCATAGTATCCGCCG	TAGTTGAGATGATGGCCCGAC
78	AATGAGATCATAGTATCCGCCG	TGTAGTTGAGCTGATGGCCC
79		
80	TGCACCAACATTGTGAACCT	GTTGAAGGTGGCTGAGGAAG
80	ATGGTTGCTCCAACATTGTGAA	AGCTCTTCGTTGAAGGTGGCT
80	ATGAAGTGTTGCTGCCACATAG	GTTGTTAGGTGGCTGAGGAAGA
81	TTGCTGCCACATAGTGAACC	TAGGTGGCTGAGGAAGAAGC
81	ATGGTTGCTCCAACATTGTGAA	AGCTCTTCGTTGAAGGTGGCT
81	ATGAAGTGTTGCTGCCACATAG	GTTGTTAGGTGGCTGAGGAAGA
82	TGCACCAACATTGTGAACCT	GTTGAAGGTGGCTGAGGAAG
82	ATGGTTGCTCCAACATTGTGAA	AGCTCTTCGTTGAAGGTGGCT
82	CAGGTTTGTTTCTACACCGTCA	GAGGCCACTGTACTCACAACAA
82	ATGAAGTGTTGCTGCCACATAG	GTTGTTAGGTGGCTGAGGAAGA
83		
84	TGTATCGGTGCCTCTATCCG	GTTGAAGGTGGCTGAGGAAG
85	GCCTCCTCAACTTGACCCTC	TTCACATCAGCGAGTCCTTG
86	GCTGCCCTCTCCCAATTC	GCTTGGGGTTGGTTTAGGA
87	GGAGACGGATAAACATGGAAAG	TACCATTCCCTCTTGCTTTGAT
87	GGAGACCGCTAAAGATGGAAAG	CCCCTTTTGCTTTGATGACTAG
88	GGGGTACAAATCCTTTTTCGTT	TAATGGGTTCCACTTGGAGAAA
89	CTTGAATCTTCCTCTGCATTCC	GCTAACTCTTCCTCCGTTGCTA
90	ACCATGGTCGCTCCATTCAC	GCTAACTCTTCCTCCGTTGCTA
91	CCGAGTTGACTCAGCTTTCTTA	GAGTGAAGGAATGGATTCGTGT
91	CTGACGAGTTGACTCAGCTTTC	GAGTGAAGGAATGGATTCGTGT
92	ATTGCGGCTAACATCTCTGG	TACGGCTGGGTTAAGGTGA
93	TCCGAGGATCACTTCTCTCTG	CCTTGCCGAACTTCTTCTTG
93	ATCTGAAGAGGAGAACCCACTG	CCTGAGATTGGATTTGAAAAC
93	GGGTGTCGTAGTTTACGGAAGA	GGATTTGAAAACGGAGAATCTG
94	CCTCCGAGGATCACTTCTCTC	CGGAGAATCTGTAGTCGTGCT
94	ATCTGAAGAGGAGAACCCACTG	CCTGAGATTGGATTTGAAAAC
94	GGGTGTCGTAGTTTACGGAAGA	GGATTTGAAAACGGAGAATCTG
94	GATCACTTCTCTCTGTTCAAGAA	GGAGAATCTGTAGTCGTGCTCC

?	AGCTGGATCCCTCTGCTCGT	AAACTCAGACCGAGTCAGATCC
95	AAGCTGGATCCCTCTGCTC	AGACCGAGTCAGATCCGAGA
96	CAAGAAGAAGTTCGGCAAGG	TGAGATTGGATTTGAAAACGG
97	AAGCTTCTTACTCCACTCGCC	GCGAGCCATTTCAGACAAGT
97	CCGACTCTCGAAGCTTCTTACT	TTTCACGACACGTGGACAAC
98	TCTACTTGTCTGAAATGGCTCG	AGAGGAAGATCTGCTCTCCGAG
98	AAACACGACAAACCGTTGTCTA	AGAGGAAGATCTGCTCTCCGAG
99	ACTACACCGACTCTCGAAGCTT	CGAGCCATTTCAGACAAGTAGA
100	GTCTCCGGTGAATCTAGGAGAG	TCATTCTTGTCACGACATTGAA
101	AAGCTTCTTACTCCACTCGCC	ATTTCACGACACGTGGACAA
102	TGCGTCATGAAGATAATTCACTA	CGGCGAGTGGAGTTAAGAAG
103	GGATGGTCATTCTCTTTGGTGT	ATCCATTAACTACAATGAAAAGGG
103	AGGAAGGTCATTCTCTTTGGTG	ATCCATTAACTACAATGAAAAGGG
104	CTCCTCCACGTAATCTCTCCTC	AAAGAATGTATCCGTGACGTCG
105	CTAGCTCTGGCAAGGAAAAGTG	TGAGCACATTAGCGCAGACAC
105	CAAGGGATAATTGCCCTAAAGA	TGAGCACATTAGCGCAGACAC
106	CTTTGAGAGGTTCTTCCCACAG	CGGTCAGATACTTTGGAAGGAA
107	TCATTTATGTATCAGGACAATGTG	TCTGTATTGAATGGATGCAACC
108	ACGCAACTGCCACCAATCAG	CCTCCATCACATCTTCAATGTC
109	TTTCCTCCTTTTATCCACAGGT	GAAAAGAGAGATGGGTACACAC
110	TATTATCGTTGAGGCTAGGGCA	GGGAGTGGGACCAAGATCCA
110	AGACTTGAGATGGCTGCGTATT	GGGAGTGGGACCAAGATCCA
111	TCCCTGGATCCATCTCAACTAT	AGAAAATGTCCTAGCCTCAACG
111	GTCCTGGACCATCTCAACTATG	GTCTAGAAATGCCCTAGCCTCA
112	GCAATTTGTGTATGTGATTCGG	TAATCTCTCCTGTGGGAGGAAG
113	AAGACGCTAAGGTAGTTGGAGG	AGCATCGTGGAGATCCTTAGTC
114	GGCATGTACTCAACGTAGCAAG	GACACTCTCAGACGATTTATTTCG
115	TATCCCGAGACTTTCCCCAT	GCTGGGTTTCGACGGTGGATGG
116	CTCACCATCGGAGAAAGAGG	TCATCACTCTCATTAACAAGATCC
117	GAACAACATCTCTTCCCTCACC	GGACCTTCCCACAACAAAAATA
118	TAGGATGCGTGTGCTAAGGC	GTTACCCTTGACACGCATGTAC
119	TCTTCAAAGCTTCTTACGAGCC	GTAGTGGACGATGGCTTGGAG
120		
121	AGGACACAGAGGCTCGAAGTTA	GAGAGTCCGGTTAAAGCCTTG
122	CCCAAAATAAATTGATGGTTTT	AACTTCTTCTTGCCAACAGGAG
122	CCCAAAATAAATTGATGGTTTT	AGGAGGCCACACCTGTTTATTA
123	CCGAAGAGTTTCCAGTGAAAAG	AGTCTCAGCAGAGCGAGATTTT
123	CGAAGGAGTTTCCAGTGAAAAG	AGTCTCAGCAGAGCGAGATTTT
124	CATCTGAAGCAGCTCTGACTTG	TTATCCACACAATCGCTAGCAC
125		
127		
128		
129		
130	ATCAGGAAGCCCATGGTACG	CCGGAGAATGGACCCAAGTACT
131		
132	ACAACTGCTGTATGATGGTAAGC	TCACATGTTCCACACAAAACAA
133	AGTCTGACTTCAAGGACTTCGC	GACGAGAGCAGAGGTTGCTAAC
133	AGTCTGACTTCAAGGACTTCGC	AAATCCGGCGATCTTGACAG
134		
135	GAGCCTGAAGGAGAGTTGGA	TGGCGATGTGTTTCATCTTC
136	CTTGGGTCCATTAGTGAGGG	TGATTTTCCTCCAATCATCAAA
137	GAAGATGAAACACATCGCCA	TCACCAACAGGATCTCCCAT
138	ACTCATAGGCGATCTGGAGTA	CTGGAGAGGAGATTCGATTTGC
139	TCTTCTGCACGCCTCACTTGTT	TTTTCCGGCGAATCCTTGAT
140	GTGTTTTTGAGGTGAAAG	AAAAAGGTATCTCCATTTGT
141	CCCGAGCCATTAGGACAAG	TTCTTACCGTGGCTTCAACC
142	CTGCACCCATCTCATCCTTT	CTGTCCCAGGAGCTTGATTC
143		
144		
145	TGAAGGCGTCGACTATCTTG	GAACTGTACGAACTGTGGCG
146	CGCCACAGTTCGTACAGTTC	CCAGTGCATAACAGTGGCAA
147	ACAATCTGAAGGCGTCCACT	CCAGTGCATAACAGTGGCAA
148	TCTTCACGGAAATCTTGCTG	CAGGCTTGTTTCGTTCAACA
149	CCTGCCCATGTCTTCAAAGT	GTCTTTCTTGTTCGGACGTG

150	GGATATTACATAATACTTGATATGCCATT	TCAAAAATAAATGTTAAAAATAAGAGGACA
150	GGATATTACATAATACTTGATATGCCA	AAGCCTATTCATATTTTCAAGTTAAT
151	GAAGTTCGAGACGCTGTCGT	CAGGGTATCCAGCCGTTG
152	GTGATTATGGCCACGTCGGCC	GAGCCCAAGGAACGGAGCGAC
153	AAAGTGCCGGTAATGTAATGGT	TGAAGGGACAACCCAATCAT
154	GGTTCGCCTCATGTTATCGTTG	GGTGGAGGTGGGGTTTATCCAA
154	ACCACTGACGTAGCACCTCC	GGTGGGGTTTTACAACGAGA
155	ACCACGAAGAAGGGAGGTTC	GTCGGAGGTGCTACGTCAGT
156	CCAATTTATCGAGCCAGACA	TGGTCCAAGCAGTTCATCAC
157	ATGCAACATCGAGCATTCTG	TCACATCCAGAGCTGACACG
158	TGGTTGCTTACTGAGAGAATGC	GACACGTGAGCAGACTCCAA
159	TGCGCTGTGCTTTATTGGGAA	CAGATTCCATTCAGACCCTAGAGG
159	CAGTGCGCTGTGCTTTATTG	CCATTCAGACCCTAGAGGCA
160	GGAGTACACTGTTACAATCACAC	AGCTGTCTATCTGTGTTGCGCTT
160	GCGCAACACAGATAGACAGC	CGGGTCTGAAGAAAAGTGGA
161	GGAGTACACTGTTACAATCACAC	AGCTGTCTATCTGTGTTGCGCTT
162	AGCGAGATCGATCCTGTTG	TCCTATGGCAGTGATGGATG
163	CGAGCAGATGGGTGCTAGTC	TGCTTTCTTAGTGGGTGAACG
164	TGAGCAAAGCAGAGACTCCA	ACCCATCTGCTCGAAGTAGC
165	AATACACGCTGCCCAGGCC	GATCTCGCTCGGTGGTTCC
165	GAATACACGCTGCCCAGG	GGCAGTGATGGATGACAACA
166	TACTAGCTCGGTGACCCGAT	ATGTGGCGAGCTTCTTTCAT
167	CAAGCAAGCAAGCTGTCTGT	GCGCGCAAACCTTTTATTAC
168	GAATCTGACCCACCCCGTTGC	AAAACCAAGAAAAAGCCAACATT
169	TGCGCGCAATAAATCAGA	TGGGTCAGATTCAGATCAGC
170	GATCTGAATCTGACCCACCC	TAACGATGAGCAAGTGCAGC
171	TCGACGTGGAAAGTATTGGA	ACAGCTGCCACTGAATCCAT
172	GCTCCTCGTGGTAGTGACGA	GACCAGAAACGCCTTGAGTC
173	CCGGCGAGGGAATACTCGAT	TCACTACCACGAGGAGCGCC
173	GCGAGGGAATACTCGATAGG	TCGTCACTACCACGAGGAGC
174	GATATGGGGTTCGGTGTCACTGA	TGGCTGCTGCTGGTGGGC
174	GTTCGGTGTCACTGACCTGT	GGCGCTGCTACTGCTGAT
175	AAATCCGCGGAAACAACAT	GCAGCTGGGTTATCCTCAAG
176	TCATCACTTGATGATATGAGTATATTCAA	CATGGTCAACTGTGAAGAAATAACATTC
177	GCTGCGTCAATCATCACTTC	TCTGTACTTGACGCCTGTGG
178	CCACAGGCGTCAAGTACAGA	TGTCAGACTCCAAGGCGAAG
179	TGACCTTGATTGCATTGCAGCTA	TGATCTTCCGGCCTTCCACG
179	CCTTGATTGCATTGCAGCTA	GGCCTTCATCCAGTTGATCT
180	GCGTCCTGCTGGTTCATTATCTG	CTTCCACGGGCTTCTTGTAGCTG
180	GCGTCCTGCTGGTTCATTAT	ATCCAGTTGATCTTCCGGC
181	CTGGTGGTGGTGCTTCTCT	ACGTGAAGATGGTCAGACAGA
182	CTGCGTGCATGTGAACATTCATG	GATAATGAACCAGCAGGACGCGA
182	ATCGACGGGTCTGTTTTCCT	ATAATGAACCAGCAGGACGC
183	TGCGTGCATGTGAACATTCATG	ACGCGAGCAGTTGTGGGTTACC
183	GATTTCATCGACGGGTCTGT	ATAATGAACCAGCAGGACGC
184	CCGACTACCCGGAGCTGAACC	TCGAAGGACGACTTGAATCTCTC
184	GACTACCCGGAGCTGAACCT	AAACAGACCCGTCGATGAAA
185	CGGAAGATCAACTGGATGAAG	GAGCTCTTCGGCGTAGTAGG
186	TGATCGCTGTCAGGGAGGGC	GTAGCGGCACCTTTTTCATGG
186	CTGATCGCTGTCAGGGAGG	CTTTTTCATGGAGCCGAGC
187	CGTTCTCTGCACTCCGATTGA	ACACACGCGCTGCCCTGC
188	CGTTCTCTGCACTCCGATTGA	GCTGCCCTGCCTCGGACC
189		
190	GGTTAAGTATGCCGAGCGCCA	TCGGCAGGAGTCAAGAGGGATAT
190	GAGCGCCAGATGAACCAG	GGCAGGAGTCAAGAGGGATA
191	GGCCAATGGATAGCCACATAGAAC	GCGCTCGGCATATTTAACTCGTGT
192	CGCATAAGTACATGACACCTCCGG	TGCGGGATTCTTGGCCGTAT
193	ACGGCTTTGGAGCTTAACGATACC	TCTGGATGGGTGCCCGGC
194	TGGTCCACAATTATCTGATGGATC	CTCGAAGCTGATCCAAGGTTG
195	CAGACAAAGTTGATGAGATATATGG	CCCAGTGCTCCATGTCTTTGAA
196	CAGCTCAAATCATAGGTCAATAAG	AAGGATAGGCTGGTTCGCTCG
197	CTCTGCTCGTGGAAGAAGTAC	ACGCGGTGGGATTCTGGATCC
198	AAATCCCCTCTACGCCCGT	CCTCTGGCACACCCCGAGAT
199	TGTGCATTCAATACGATCAGCCA	ATGTTTTTGCTGATGTTGCACAG

199	GTGCATTCAATACGATCAGC	TGAATTGGACCTGCTCTTTT
200	AAAGAGCAGGTCCAATTCAG	GACTGTACGCAGAGTTTTGTGTAG
201	GATCGAAGGCCTGACCGGT	GAAAGGCGATGTAACGCGG
201	GAAGCGATCGAAGGCCTGA	TGGGAAAGGCGATGTAACG
202	ACCATGTTAATGTCACTTTTTAGTGG	GATATATTCCCTACGAGGAATGTC
202	CATTGTGAGGAaCACCATGTTAATG	ATATTTGTCCCTAAACCTCGGGATAT
203	GGATTAATACTTTTGGACATGTTTG	ATATGGTGCGAACAACTCAACAGTA
203	TTTGACATGTTTCTTAATTTTTATAG	GAACCCTCAACAGTAATAGCAATCAT
204	TCTACCTCTGAGATACATTCATTTAA	TATAAGGATAAATGTCCTACTTTTCT
205	GAGGGTTCGCACCATATCATG	CCATTTTGAGGCGGCATTCC
205	TATTACTGTTGAGGGTTCGCAC	AACCATTTTGAGGCGGCATT
206	TGGCCATTGTAGATATAATATGAT	TCGAAGGAGATAAGAAAGATCAAA
207	GGGGATATTATGTAGGACTTGGAG	CACCAAAATATCAACAGAGGCATG
208	CCTTGGCAGACAACAGACAGATCA	TTTGACTGGGAGTAAATGCAAGC
208	TGGCAGACAACAGACAGATCA	GGGATTTTCGGGACTGAGTT
209	TTGTTTTGTTTTTCCTTGGCAGAC	TTCGGACTGGGAGTAAATGCA
210	ACTCAAAGTGGTGCAATCGCAA	CGATACGGACCACGGCAAGC
210	ACCGGGAGACAAGAGAGAAACT	GATACGGACCACGGCAAGC
211	AGACAGATCAGTAAATCACGCATG	GGGATTTTCGGGACTGAGTTTGAC
211	AGACAGATCAGTAAATCACGCATG	TTGGGATTTTgGGGACTGAG
212	TTTGAATGAATTGAAGCTCTGAA	TTTCAATTGTTGCATCTCGAGTT
212	TTTTGAATGAATTGAAGCTCTG	TCTCGAGTTTTGTAGGAAGCAG
213	ATCCTCTGCTAAAAAAACCCATT	TCGAGTTTTGTAGGAAGCAGTTT
214	ACCGGACTCCTTTCCAATGTC	TCAGTATGTGGGGATTCAAAC
215	AATGGCAACTTGTATCGGCTAG	CATGTTACCTATTAGAGCACTGAG
216	GAGTGCAGAACCTGATGGGT	GTACTGGCTGAAGAAGCCGA
217	TGCAGTCAGGGTTTTTTTATCAAC	AGCTCAGGCATTCAGGTAGATC
218	CCTTGTGGAATGTTGCTGTTAT	ACGACGGACACTGAAGAGGCT
219	TCTTCAGTGTCCGTCGTAGC	CCCTTTCTCCCTGCTCCAT
220	CCGGGCGAGGGGGTGGTC	GCTTGCTCGCTGCTCGGGC
220	CAGGGGAGGGGGTGGTCGC	GTGTGCTTGCTCGCTGCTC
221	TCCGAGCCCACAAATCTGTAC	CAAATTAACGCTGGAAAGTTTGAA
222	ATATTACCCGTAGGTGACAAA	CAGGAAGGTCTTGAGGAAGCT
222	CGTAGGTGACAAAGGGTTCAA	AGGAAGGTCTTGAGGAAGCTA
223	AGCTTGTCTTCGCTTGGTAGC	TTCACAACCCAAAGCCCTG
223	AGCTTGTCTTCGCTTGGTAGC	CCTGTGGCCGGTAAAAGTATA
224	GCGAAAAAACCAAGAAAGATTA	ATCTGGGCAACAACACACACTTT
225	CTGCGAAAAACCAAGAAGATTA	ATCATCTGGCACACACACTTTG
226	TGAGAACAATGAGACACACGAATT	GTACAGAATTGTGGAGTTCCATG
226	CGAATTAAGTGAAGATGCCCAAA	GTACAGAATTGTGGAGTTCCATG
227	GCCTGATTCGGGTCTGTATGC	TGCATCACCAATTCACCAGTT
228	TGACTCGGCTCAATTCCAG	ATGAAAGTGACGAGTGGATG
229	CGGTAGCTATGCACAGATTG	TGCATTCAAATGGACAGAACTG
230	CTAGTAAGGTGTGGCTTGGTTGAC	CGAAACTAACACCGTCAAACTCTA
230	GTGGCTTGGTTGACCTTGAGG	CGAAACTAACACCGTCAAACTCTA
231	TCCGAACGCCGCCGAGAGC	GGCAGGCAGGCACGCACAT
231	TCCGAACGCCGCCGAGAGC	GGCAGGCAGGCACGCACAT
232	GTGAGGCGAAGTACATGGCG	AGCCACATCACCTAAGCAGC
233	GCGCGTCGGTTCTAAACATA	AACCAGCTGTGCTCGAGATGA
234	ACTTCTATTTCCAAGCTAACAACC	TTTCCAGGATGTTGGGACC
235	TAAATTAAAGCCTCATGTGCA	TTCTTTGTGTCAGGGGCTCAT
236	GGTGTGTGCTCCAAGTGTGT	AAGCACTTGCAGAGGCTGTT
237	TCTAACTCAGCAAGCCTCCAAG	CTACACACTTGGAGCACACACC
238	GTTGACCAGCTGTGATTTCG	ACTCGTGGTCGTGGAATACA
239	GCCTCTGCAAGTGCTTAATTGTA	GTCGTGGTCGTGGAATACATCG
239	TTGAACAGCCTCTGCAAGTG	CATCGAAATCACAGCTGGTC
240		
241	ACACAGTGCTTCCGTAAACC	CATCGAAATCACAGCTGGTC
242	CACAGTGCTTTCGTAAACCTAGA	TGGTCGTGGAATACATCGAA
243	ATGAACGAAAGAGCGAGATA	GGCCGTATACTTGCTCATCG
244	AATAGCTCAGCTGCCGGAGT	AGCAGCAGCAGTGCATGG
245	GGTTGGTAATTTCAGAGCTAGA	TCGAATGGCGTGTACCACAGTA
246	CGATGGGTTTTCACAACTCA	GTAACCTAGAATCCACATCAAAGC
247	CCATCTCTTTACAGTAAATATCCG	GACTGTTCTTTGAAATGAGGAT

248	CCATCTCTTTACAGTAAATATCCG	GACTGTTCTTTGAAATGAGGAT
249	ATGCCTTTACTGATTGGGTTACA	GTTTTTTGGAAGGAGTAATAGATT
250	CAGAAGGTCTGTTCGTTCCA	TGACTGTTCTTTGAAATGAGGA
251	GCTACGCCATTTAGCGAATTT	GTGGGAGGATAAAAAAGATATTGCT
251	AGCGAATTTGGGAAAATCAA	GAAGACAATGGTGGGAGGAT
252	TATAATGTTTAGCGACAGGGATG	TAGCTCATTATTGCCTTCCGTAG
252	TAGCGACAGGGATGTCGAG	AGCTCATTATTGCCTTCCGT
253	GCACGCACGTCGTTGGTGA	TCGACAAGCACCCGTACCGC
253	GCACGTCGTTGGTGAAGAAG	GGTGTACCCCGTCGACAA
254	GCACGTCGTTGGTGAAGAAG	GTCGACAAGCACCCGTACC
255	TCAGGTACACGGGGAAGTCGG	GCGCGGTGGTGGTGAAGAA
255	CTCAGGTACACGGGGAAGTC	CGGTGGTGGTGAAGAACC
256	CCCAGCGCCTCGTCCCAGATC	GTGGGCAGCGGGGACAGCGAG

WHAT IS CLAIMED IS:

1. A nucleic acid segment comprising at least 10 contiguous nucleotides including a polymorphic site from a sequence shown in Table 1 or Table 2, or a plant cognate variant thereof, or the complement of the segment.

2. The nucleic acid segment of claim 1, wherein the segment is less than 100 bases.

3. The segment of claim 1 that is less than 50 bases.

4. The segment of claim 1 that is less than 20 bases.

5. The nucleic acid segment of claim 1, wherein the segment contains at least 10 contiguous nucleotides including a polymorphic site from a sequence shown in Table 1.

6. The nucleic acid segment of claim 5, wherein the sequence is a Brassica sequence.

7. The nucleic acid segment of claim 5, wherein the sequence is a corn sequence.

8. The nucleic acid segment of claim 1 that is DNA.

9. The nucleic acid segment of claim 1 that is RNA.

10. The segment of claim 1, wherein the polymorphic site is diallelic.

11. An allele-specific oligonucleotide that hybridizes to a sequence shown in Table 1 or 2, or its complement.

12. The allele-specific oligonucleotide of claim 11 that is a probe.

13. The allele-specific oligonucleotide of claim 11, wherein the a central position of the probe aligns with the polymorphic site in the sequence.

14. The allele-specific oligonucleotide of claim 11 that is a primer.

15. The allele-specific oligonucleotide of claim 11, wherein the 3' end of the primer aligns with the polymorphic site of the segment.

16. A method of analyzing a nucleic acid, comprising: obtaining the nucleic acid from a plant, and determining a base occupying any one of the polymorphic sites shown in Table 1 or 2.

17. The method of claim 16, wherein the determining comprises determining a set of bases occupying a set of the polymorphic sites shown in Table 1.

18. The method of claim 17, wherein the nucleic acid is obtained from a plurality of plants, and a base occupying one of the polymorphic positions is determined in each of the subjects, and the method further comprises testing each plant for the presence of a phenotype, and correlating the presence of the phenotype with the base.

19. Use of a polymorphism shown in Table 1 or 2, a nucleic acid segment of claim 1, or an allele-specific oligonucleotide of claim 11 to determine common or disparate ancestry between two or more plants.

20. Use of a polymorphism shown in Table 1 or 2, a nucleic acid segment of claim 1, or an allele-specific oligonucleotide of claim 11 in plant breeding.

21. Use according to claim 20, wherein the polymorphism, nucleic acid segment or allele-specific

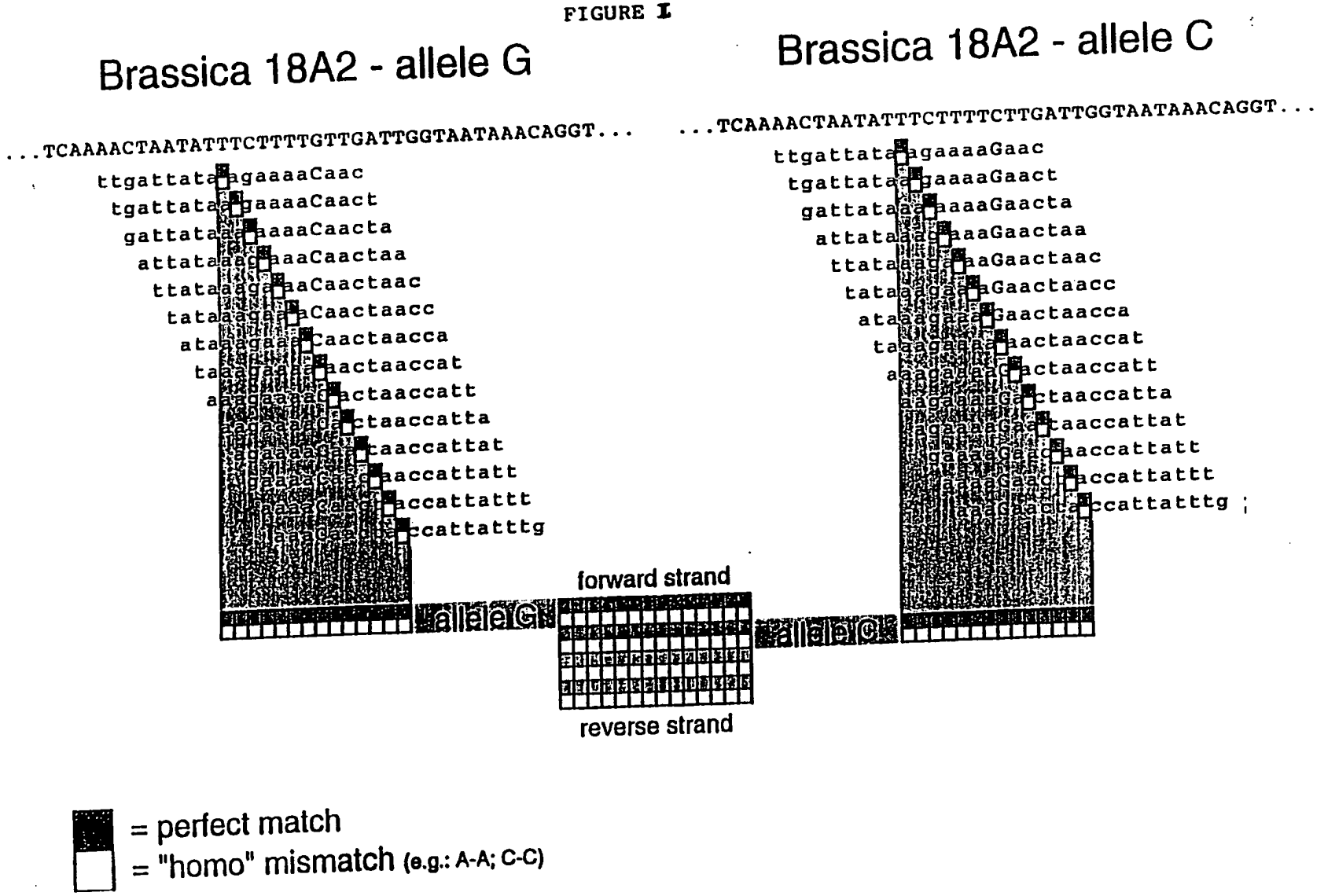
oligonucleotide is used to monitor a genetic contribution of an ancestral plant to a progeny plant.

22. Use of a polymorphism shown in Table 1 or 2, a nucleic acid segment of claim 1, or an allele-specific oligonucleotide of claim 11 to trace progeny of a proprietary plant.

23. Use of a polymorphism shown in Table 1 or 2, a nucleic acid segment of claim 1, or an allele-specific oligonucleotide of claim 11 in certification of a hybrid plant.

24. Use of a polymorphism shown in Table 1 or 2, a nucleic acid segment of claim 1, or an allele-specific oligonucleotide of claim 11 to identify a progeny of a backcross of a selected plant with an ancestral plant having a desired genetic contribution from the ancestral plant.

FIGURE 1


Brassica 18A2 - allele G
...TCAAAACTAATATTTCTTTTGTTGATTGGTAATAAACAGGT...
Brassica 18A2 - allele C
...TCAAAACTAATATTTCTTTTCTTGATTGGTAATAAACAGGT...
forward strand
reverse strand
= perfect match
= "homo" mismatch (e.g.: A-A; C-C)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US97/21782

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) :C07H 21/00, 21/02, 21/04; C12N 15/09; C12Q 1/68
US CL :435/6, 172.3; 536/23.1, 24.3

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/6, 172.3; 536/23.1, 24.3

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Databases:APS, Medline, Biosis, Genbank
Search Terms:Brassica; polymorph?; restriction; fragment?; length; rflp; lemieux?/au; landry?/au; sapolsky?/au

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	CROSS et al. Purification of CpG islands using methylated DNA binding column. Nature Genetics. March 1994, Vol. 6, pages 236-244, see entire document, especially sequences.	1-24
Y	OHNUMA et al. Archaebacterial Ether-linked Lipid Biosynthetic Gene: Expression Cloning, Sequencing, and Characterization of Geranylgeranyl-Diphosphate Synthase. Journal of Biochemistry. 20 May 1994, Vol. 269, No. 20, pages 14792-14797, see entire document, especially sequences.	1-24
Y	AHOUSE et al. Mouse MHC Class I-Like Fc Receptor Encoded Outside the MHC. Journal of Immunology. 01 December 1993. Vol. 151, No. 11, pages 6076-6088. See entire document, especially sequences.	1-24

[X] Further documents are listed in the continuation of Box C. [ ] See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search
19 MARCH 1998

Date of mailing of the international search report
29 APR 1998

Name and mailing address of the ISA/US
Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231
Facsimile No. (703) 305-3230

Authorized officer
BRIAN R. STANTON
Telephone No. (703) 308-0196

Form PCT/ISA/210 (second sheet)(July 1992)*

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US97/21782

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WILSON et al. 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans. Nature. 03 March 1994, Vol. 368, pages 32-38, see entire document, especially sequences.	1-24
Y	SAIKI et al. Analysis of enzymatically amplified β-globin and HLA-DQα DNA with allele-specific oligonucleotide probes. Nature. 13 November 1986, Vol. 324, pages 163-166, see entire document.	1-24
Y	PURDY et al. Cloning, nucleotide sequences and characterization of a gene encoding superoxide dismutase from Campylobacter jejuni and Campylobacter coli. Microbiology. 1994, Vol. 140, pages 1203-1208, see entire document, especially sequences.	1-24
Y	GUSELLA, J.F. DNA polymorphism and human disease. Annual Review of Biochemistry. 1986, Vol. 55, pages 831-854, see entire document.	1-24
Y	LOK et al. The nucleotide sequence of the 5' end of Papaya Mosaic Virus RNA: Site of in vitro Assembly initiation. Virology. 1986, Vol. 153, pages 289-296, see entire document, especially sequences.	1-24
Y	WHARTON et al. Nucleotide sequence from the neurogenic locus Notch implies a gene product that shares homology with proteins containing EGF-like repeats. Cell. December 1985, Vol. 43, pages 567-581, see entire document, especially sequences.	1-24
Y	BOARDMAN et al. Regulation of expression of a Xenopus borealis embryonic/larval alpha3 skeletal-actin gene. European Journal of Biochemistry. 1992, Vol. 208, pages 241-249, see entire document, especially sequences.	1-24

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US97/21782

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-24 (in part)

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US97/21782

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING
This ISA found multiple inventions as follows:

This application contains claims directed to more than one species of the generic invention. These species are deemed to lack Unity of Invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. The species are as follows:

Each of the 1282 sequences listed in Tables 1-3 are a separate species because there is no requisite structural relationship between the species. Therefore, the species cited above do not relate to a single inventive concept under PCT Rule 13.1 because under PCT Rule 13.2, the species lack the same or corresponding special technical feature. There is no structural relationship between the separately recited sequences.

Applicant is entitled to have ten (10) specified sequences searched and no more than four (4) additional sequences search for each additional fee. Since no fee has been paid, the first ten (10) sequences listed in Table 1 have been searched.